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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 21, 2004, 09:59:59; Search time 13 Seconds (without alignments) 640.863 Million cell updates/sec

US-10-031-607-7 913 1 MVRLPLQCVLWGCLLTAVHP......WLCNRQAQTRLMLSVVPRIG 160 Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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SUMMARIES		- QI		TNR5 BOVIN	TNR5 MOUSE	TR11_MOUSE	TR11 HUMAN		TR14 HUMAN					T11B_HUMAN	T11B MOUSE	TR1B MOUSE	CRMB_VARV	TNR6_BOVIN	CRMB CAMPS	TNR6_PIG	TNR6 HUMAN		CRMB COWPX		TNR3_MOUSE			TNR4 MOUSE	TNR4 HUMAN	TR16_CHICK	TR1A RAT	VT2 MYXVL	TR1A_MOUSE	TR1A_HUMAN	TR25_HUMAN
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Q14162 homo sapien 095407 homo sapien P25943 shope fibro P08138 homo sapien 0920w1 mus musculu 090wy2 oryzias lat P5055 sus secrefa P07174 rattus norv P10041 drosophila P11046 drosophila p99566 homo sapien 019131 bos taurus
SREC HUMAN TR6B—HUMAN TR6B—HUMAN TR1G—MOUSE TR1G—MOUSE TR1G—NOUSE TR1G—RAT TR1A—BOVIN
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830 320 325 427 417 514 461 461 1790 1587
133.6 122.7 122.7 122.0 122.0 111.7 11.6
124 122 115 116.5 114.5 110.5 109.5 108.5 107 107
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## ALIGNMENTS

RESULT 1  THES HUMAN  STANDARD; PRT; 277 AA.  AC 252942; QBSVUO,  10-MAY-1992 (Rel. 22, Created)  DT 01-MAY-1992 (Rel. 22, Last sequence update)  DT 15-MAR-2004 (Rel. 22, Last sequence update)  DT 15-MAR-1992 (Rel. 22, Last sequence update)  DT 15-MAR-1992 (Rel. 22, Last sequence update)  DT 15-MAR-1992 (Rel. 31, Last sequence update)  DE TUDIOR DESCRIPTION (Rel. 31, Last annotation update)  NEMBRA-1992 (Rel. 32, Carariates, Carariatis, Vertebrata, Euteleostomi;  ON STATE DESCRIPTION (Rel. 31, Last annotation)  NEMBRA-1992 (Rel. 31, Last annotation (Rel. 31, Rel.	ate)  vember 5 precursor  CD40) (CDw40) (Bp50).  ertebrata; Euteleostomi;  Hominidae; Homo.  ded to the nerve growth  in carcinomas.";  L.M., Beare D.M.,  degeman A.M., Brown A.J.,  r.C., Carter N.P.,  N., Clark S.Y., Clee C.M.,  or R.E., Corby N.R.,  or R.E., Corby N.R.,  with P.D., Dunn M., Hewden P.U.,  Rench L., Garner P.,  r., Holden J.L., Howden P.J.,  K., Johnson C.M., Johnson D.,  s. A., Laird G.K., Lovell J.D.,  McLay K., McMurray A.A.,	Mailin S.A., Mistry D., Moore M.J.F., Mullikin J.C., Mickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingma S.R., Plumb R.W., Ramsay H., Phillimore B.J.C.T., Prathalingma S.R., Plumb R.W., Ramsay H., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N. Taylor R., Tee L., Thomas D.W., Thorpe A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A. Wilming L., Whittaker P., Willey D.L., Williams L., Williams S.A. Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S. Rogers J.,
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ID-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
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PDB;
PDB;
  MEDLINE=2288257; PubMed=12477932;
Mature R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buttow K.H., Schemen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B., Buttow K.H., Schemen C.M., Schuler G.D.,
Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenoko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Soares M.B., Bonaldo M.F., Cazninci P., Prange C.,
Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wille B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Worley Y.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley V.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,
Fabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Cheneration and mouse cDNA sequences.",
Ill "Generation and initial analysis of more than 15,000 full-length
Human and mouse cDNA sequences.",
Fellow D. Nellow S.C., U.S. Boufford C.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH TRAFS.

MEDIATE=8912745; PubMed=9511754;

MAIZUSHE=8912745; PubMed=9511754;

Otsuka M., Yamamoto T., Inoue J. I.;

Cloring and Characterization of a cDNA encoding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAFS).";

Gene 207:135-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95184010; PubMed=7533327;
Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.;
"Involvement of CRAF1, a relative of TRAF, in CD40 signaling.";
Science 267:1494-1498(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-STRUCTURE MODELING OF 24-144.
MEDLINE=97189482; PubMed=9037712;
MEDLINE=97189482; PubMed=9037712;
"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40.";
[11]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95129692; PubMed=7530216; Sato T., Trie S., Reed J.C.; Racd J.C.; Trie S., Reed J.C.; An novel member of the TRAP family of putative signal transducing proteins binds to the cytosolic domain of CD40.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "CD40-tumor necrosis factor receptor-associated factor (TRAF) interactions: regulation of CD40 signaling through multiple TRAF binding sites and TRAF hetero-oligomerization."; Biochemistry 37:11836-11845 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH TRAF1; TRAF2; TRAF3 AND TRAF5.
MEDLINE=98384149; PubMed=9718306;
Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
alternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001)
                                                                     SEQUENCE FROM N.A. (ISOFORM I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 358:113-118(1995).
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MEDLINE=98266353; PubMed=9605317; Singh J., Garber B., van Vljmen H., Karpsusas M., Hsu Y.-M., Zheng Z., Naismith J.H., Thomas D.; "The role of polar interactions in the molecular recognition of CD40L with its receptor CD40.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRAF3.
MEDLINE=22000222; PubMed=12005438;
Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
Satterthwait A.C., Cheng G., Ely K.R.;
"Downstream regulator TANK binds to the CD40 recognition site on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insoid=P25942-2; Sequence=VSP 006472, VSP 006473;
-!- TISSUB SPECIFICITY: B-cells and in primary carcinomas.
-!- DISEASE: Defects in TNFRSFS are the cause of hyper-IgM immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an autosomal recessive disorder which includes an inability of B cells to undergo isotype switching, one of the final differentiation steps in the humoral immune system, an inability to mount an antibody-specific immune response, and a lack of
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20442386; PubMed=10984535; Nu H., Reed J.C., Bly K.R.; Lao E., Chiou C.K., Wu H., Reed J.C., Bly K.R.; "Molecular basis for CD40 signaling mediated by TRAF3."; Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21532985; PubMed=11675497;

Ferrari S., Giliani S., Insalaco A., Al-Ghonaium A., Soresina A.R. Loubser M., Avanzini M.A., Marconi M., Badolato R., Ugazio A.G., Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D., Plebani A.;

Findations of ChO gene cause an autosomal recessive form of immunodeficiency with hyper IgM.";

Froc. Natl. Acad Sci. U.S.A. 98:12614-12619(2001).

-! FUNCTION: Receptor for TNFSF5/CD40L.

-! SUBGELLULAR LOCATION: Type I membrane protein (isoform I);

secreted (isoform II).
                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
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SIMILARITY: Contains 4 TMPR-Cys repeats.
DATABASE: NAME-PROW, NOTE=CD guide CD40 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                       Protein Sci. 7:1124-1135(1998).
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26-SEP-01.
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1FLL; 18-OCT-00.
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TNRS MOUSE
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SEQUENCE
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Best Local
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                                                                                                                                   9
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                                                                                                                                   1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunology 90:294-300(1997).
-!- FUNCTION: Receptor for INFSF5/CD40L.
-!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: 4 INFR-Cys repeats.
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Released annotation update)
10-OCT-2003 (Released annotation update)
10-OCT-2003 (Released annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] SEQUENCE FROM N.A. MEDWED=9135560; SEQUENCE FROM W.C., Estes D.M.; Hirano A., Brown W.C., Estes D.M.; Hirano A., Eronna, W.C., Estes D.M.; "Cloning, expression and biological function of the bovine CD40 homologue: role in B-lymphocyte growth and differentiation in
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                         Score 785; DB 1; Length 277;
Pred. No. 5.7e-65;
1; Mismatches 6; Indels
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InterPro; IPR008063; Fas_receptor.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 4.
PRINTS; PR01680; FASECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS00652; TNFR_NGFR_1; 1.
IPROSITE; PS00652; TNFR_NGFR_1; 1.
IPROSITE; PS00652; TNFR_NGFR_1; 1.
IPROSITE; PS0050; TNFR_NGFR_1; 1.
IPROSITE PS0050; TNFR_1; 1.
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CYTOPLASMIC (POTENTIAL)
TWFR-CYS 1.
TWFR-CYS 2.
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                              86.0%;
95.1%;
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                                                  Best Local Similarity 95.1
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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TOTIES R.M., Clark E.A.;
"Differential increase CD40 upon B lymphocyte activation.";
J. Immunol. 148:620-626(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P275<u>12;</u> Q99NEO; Q99NEI; Q99NEZ; Q99NEZ;
01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last sention update)
11-OCT-2003 (Rel. 42, Last sention update)
12-OCT-2003 (Rel. 42) (Ast Sequence (Comparison Comparison (CD40L receptor) (B-Cell surface antigen CD40) (BFSO) (CDw40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM I).
STRAIN=BALB/c; TISSUE=Liver;
STRAIN=93094586; Pubmed=1281194;
Grinaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
Howard M., Cockayne D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.1%; Score 558; DB 1; Length 269; 69.6%; Pred. No. 3.4e-44; ive 12; Mismatches 29; Indels
144 TURE-CYS 3.

187 TURE-CYS 4.

37 BY SIMILARITY.
51 BY SIMILARITY.
59 BY SIMILARITY.
103 BY SIMILARITY.
119 BY SIMILARITY.
116 BY SIMILARITY.
116 BY SIMILARITY.
117 BY SIMILARITY.
118 BY SIMILARITY.
119 BY SIMILARITY.
110 BY SIMILARITY.
111 BY SIMILARITY.
112 BY SIMILARITY.
113 N-LINKED (GLONAC. ..) (POTE 180 N-LINKED (GLONAC. ..) (POTE 269 N-LINKED (GLONAC. ...) (POTE
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Torres R.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
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Nature 390:175-179(1997).
[2]
SEQUENCE FROM N.A.
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                                                                                                                              D.I., Lederman S., Baltimore D.; TRAF, in CD40 signaling.";
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REMBL; M94126; AAA3404.1; -.

REMBL; M94129; AAA3404.1; -.

REMBL; M94129; AAA3404.1; JOINED.

REMBL; M94127; AAA3404.1; JOINED.

REMBL; AA401389; CAC29428.1; -.

REMBL; AA401389; CAC29428.1; -.

REMBL; AA401389; CAC29429.1; -.

REMBL; AA401389; CAC29429.1; -.

REMBL; AA401389; CAC29430.1; -.

REMBL; AA401389; CAC29429.1; -.

REMBL; AA401389; CAC29429.1; -.

REMBL; AA401389; CAC29429.1; -.

REMBL; AA601389; CAC29429.1; -.

REMBL; AA601389; CAC29429.1; -.

RESP; PESP$2542; ICDF.

MGD; MGI: 88336; TNFR C6.

REMRT; REMOSOS TNFR C6.

REMRT; REMOSOS TNFR C6; A.

REMRT; REMOSOS; TNFR NGFR 1; 1.

REMSITE; PSOMOSOS; TNFR NGFR 1; 1.

REMSITE; PSOMOSOS; TNFR NGFR 2; 4.

RECEPTOR; Transmembrane; Glycoprotein; Repeat; Signal;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P27512-4; Sequence=VSP_006479, VSP_006480;
                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=5;
Name=1;
 Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isold=P27512-5; Sequence=VSP 006476;
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P27512-1; Sequence=Displayed;
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                                                MEDLINE=95184010; PubMed=7533327;
Cheng G., Cleary A., Ye Z.S., Hong
"Involvement of CRAF1, a relative of
Science 267:1494-1498(1995).
                                   INTERACTION WITH TRAFS.
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SIGNAL 1
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KKVVKKKPKDNEMLPPARR -> SECSGEEREGGFSPVEPA S (in isoform III).
/FIId=VSP_006477.
Missing (in isoform III).
/FIId=VSP_006478.
KKVVKKP -> SQGFTKG (in isoform IV).
/FIId=VSP_006479.
BY SIMILARITY.
CHUNKED (GLCNAC. . . ) (POTENTIAL).
RECENTIALLY (GLCSLKSRMALLVIPVNG SCEDKNILEVLQKGTSGTNVICGLKSRMALLVIPVNG PREKVPDASPAGHSCRDGHPHHFRGVSLYQKGGGGTKG
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                                                                                                                                                                                                                                                                                         /FIId=VSP 006474.
Missing (In isoform II).
/FIId=VSP 006475.
GLKSRWRALLVIPVVMGILITIFGVFLYIK -> E (in
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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035305; 08VCT7;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 48, Last annotation update)
10-0CT-2003 (Rel. 48, Last annotation update)
10-0CT-2003 (Rel. 48, Last annotation update)
10-0CT-2003 (Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (ODFR).
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TISSUE=Fetal liver;
MEDLINE=98032977, PubMed=9367155,
Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.9%; Score 483; DB 1; Length 289; 54.9%; Pred. No. 2.6e-37;
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P_006480.
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/FTId=VSP
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TNFRSF11A OR RANK.
Mus musculus (Mouse)
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TISSUE=Mammary gland;

MEDLIKE=22388257; PubMed=12477932;

A Strausberg R.L., Feligold E.A., Gruse L.H., Derge J.G.,

A Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Hanna and mouse cDNA sequences.";

Human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Makagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K., Morinaga T., Higashio K.; Maraguchi K., Shima N., Yasuda H., Yano K., Morinaga T., Higashio K.; In signaling receptor for osteoclast differentiation factor in osteoclastogenesis."; Biochem. Biophys. Res. Commun. 253:395-400(1998).

-!-FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OFG1; essential for RANKL-mediated osteoclastogenesis. Involved in the regulation of interactions between T-cells and dendritic cells.

-!-SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SUBCELUILAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: UDIQUITOUS EXPRESSION WITH HIGH LEVELS IN
TRABECULAR BONE, THYMUS, SMALL INVESTINE, LUNG, BRAIN AND KIDNEY.
WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP019046; AAB86810.1; --
EMBL; BC019185; AAH19185.1; --
EMSP; P25942; 1CDF.
MGD; MG1.1314891; Thfrafila.
GO; GO:0007275; P:development; IMP.
GO; GO:0007515; P:1ymph gland development; IMP.
GO; GO:001503; P:ossification; IMP.
InterPro; IPRO1368; TWFR c6; 3.
SWART; SM0208; TWFR c6; 3.
SWART; SM0208; TWFR, 4.
PROSITE; PS50055; TWFR NGFR 1; 1.
PROSITE; PS50055; TWFR NGFR 2; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Contains 4 TNFR-Cys repeats.
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
BY SIMILARITY.
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             RANGE OF THE LEAD BY A BARRAR BARRAR
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                                                                                                                                                                                                                    8 CVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTBFTETECLPCGESEF 67
                                                                                                                                                                                                                                               77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakagawa N., Kinosaki M., Yamaguchi K., Shima N., Yasuda H., Yano K., Morinaga T., Higashio K., Maraguchi K., Store K., Respective Seculation Signatural signatural receptor for osteoclast differentiation factor in osteoclastogenesis.";

Biochem. Biophys. Res. Commun. 253:395-400(1998).
                                                                                                                                                                                                                                              19 CVLLVPLOVTLOVTPP-CTQERHYEHLGRCCSRCEPGKYLSSKCTPTSDSVCLPCGPDEY
                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The TRAF family of signal transducers mediates NF-kappaB activation
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
R -> K (IN REF. 2).
R -> K (IN REF. 2).
W, FRC1872E99511DSE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-027-2001 (Rel. 40, Created)
16-027-2001 (Rel. 40, Last sequence update)
10-027-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 11A precursor (Receptor activator of NF-KB) (Osteoclast differentiation factor receptor) (OpF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS, VARIANT PDB2
ALA-LEU-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS, AND VARIANT VAL-192.
MEDLINE=20082806; PubMed=10615125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6. MEDLINE=98447691; PubMed=9774460; Wong B.R., Josien R., Lee S.Y., Vologodskaia M., Steinman R.M., Choi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Dendritic cell;
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Naraskovsky B., Billingsley W.L., Dougall W.C.,
Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
Galibert L.;
                                                                                                                                                              Length 625;
                                                                                                                                                                                          66; Indels
                                                                                                                                                            28.7%; Score 262; DB 1; 38.2%; Pred. No. 9.6e-17;
                                                                                                                                                                                          16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the TRANCE receptor.";
J. Biol. Chem. 273:28355-28359(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99097247; PubMed=9878548;
                                                                                                                                  66621 MW;
                                                                                                                                                                                                                                                                                                                                       128 GFGVKQIAVRPKTWLC 143
                                                                                                                                                                                                                                                                                                                                                                   137 ĠPĠAQHPLQLNKDTVĊ 152
                                                                                                                                                                                          52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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494
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   Similarity
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Best Local
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SEQUENCE FROM N.A.
TISSUE=PNS;
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TRIB HUMAN

AC P203338

DT 28-FEB-
DT 28-FE
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                                                                                                                                                                                                                                                             gland.

-!- DISEASE: Defects in TNPRSF11A are the cause of familial expansile osteolysis (FEO) [MIM.174810]. FEO is a rare autosomal dominant bone disorder characterized by focal areas of increased bone remodaling. The osteolytic lesions develop usually in the long bones during early adulthood. FEO is often associated with early onset deafness and loss of dentition.

-!- DISEASE: Defects in TNPRSF11A are a cause of paget disease of bone. DISEASE: Defects in TNPRSF11A are a cause of paget disease of bone. PDE2 is a bone remodelling disorder with clinical similarities to FEO. Unlike FEO, however, affected individuals have involvement of the axial skeleton with lesions in the spine, pelvis and skull.

-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                         familial expansile osteolysis.";

Nat. Genet. 24:45-48(2000).

-!- FUNCTION: Receptor for TNFSF11/RANKL/TRANCE/OPGL; essential for FANKL-mediated osteoclastogenesis. Involved in the regulation of interactions between T-cells and dendritic cells.

-!- SUBGNIT: Interacts with TRAFF1, TRAFS, TRAFF5 and TRAFF.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Ubiquitous expression with high levels in skeletal muscle, thymus, liver, colon, small intestine and adrenal
                                       Anderson D.M.; "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM, 602080; --
GO; GC:0004872; F:receptor activity; TAS.
GO; GC:0007267; P:cell-signaling; TAS.
GO; GC:0007267; P:cell-signaling; TAS.
GO; GC:0007165; P:signal transduction of cell proliferation; TAS.
Interpro; IPR001368; TNFR_c6.
Interpro; IPR001368; TNFR_c6.
FAM: PR00209; TNFR c6; 4.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
TURR-CYS 1.
TURR-CYS 2.
TURR-CYS 4.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
L -> LALLLICALL (in PDB2).
Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H., Mallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUPERFAMILY MEMBER 11A. EXTRACELLULAR (POTENTIAL).
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Genew; HGNC:11908; TNFRSF11A.
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SIGNAL 1 29
CHAIN 30 616
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CARBOHYD
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64 ESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 PDEYLDSWNEEDKCLLHKVCDTGKALVAVVAGNSTTPRRCACTAGYH-WSQDCECCRRNT 131
                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 LLLLCALLARLQVALQIAPP-CTSEKHÝEHLGRCCNKČEPGKYMSSKCTTTSDSVČLPCG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P20333; Q16042; Q9UHI;
01-FB2-1991 (Rel. 17, Created)
28-FB2-2003 (Rel. 41, Last sequence update)
15-MRA-2004 (Rel. 43, Last sequence update)
Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept) (Contains: Tumor necrosis factor binding protein 2 (TBPII)]
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                         4 LPLOCVLWGCLLTAVHPEPPTACREKOYLINSQCCSLCQPGQKLVSDCTEFTETECLPCG
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MEDIATE=9050659; PubMed=2160731;
Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
Dower S.K., Cosman D., Goodwin R.G.;
"A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins";
Science 248:1019-1023(1990).
                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=96299745; PubMed=8661109;
Beltinger C.P., White P.S., Maris J.M., Sulman B.P., Jensen S.J.,
Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
                                                                                                                                                                                                                                                                                                                      5
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MEDLINE-91045-991; PubMed-2172983;
KODHO T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
"A second tumor necrosis factor receptor gene product can shed
naturally occurring tumor necrosis factor inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
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                                                                                                                                                                                                                                           28.4%; Score 259; DB 1; Length 616; 37.9%; Pred. No. 1.8e-16; Live 17; Mismatches 68; Indels
                                                                                                        A -> V. _
/FTId=VAR_011518.
E3DE9A7A08196F81_CRC64;
                                 L -> LLLCALL (in FEO).
/FTId=VAR_011517.
FTIG=VAR_011516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 ECAPGLGAQHPLQLNKDTVC 151
                                                                                                                                                                            66033 MW;
                                                                                                                                                                                                                                                                                                                      53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                            616 AA;
                                                                                                                                                                                                                                                                                    Sest Local Similarity
                                                                                                    192
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MEDLINE=22388257; PubMed=12477932;

Strausberg R.L. Feingold E.A. Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Distribench M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raba S.G., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

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Rodriguez A., Schein J.E., Jones S.J.M., Marra M.A.;

Romerzation and initial analysis of more than 15,000 full-length

Runnand mouse cDNA sequences.";
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MEDLINE=90110215; PubMed=2153136;
Engelmann H., Novick D., Wallach D.;
Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface
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Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
Lipari M.T., Goeddel D.V.;
"Blochemical properties of the 75-kDa tumor necrosis factor receptor
Characterization of ligand binding, internalization, and receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R., Brockhaus M., Lesslauer W., Tasslauer W. Tracestors have similar extracellular, but distinct intracellular, domain sequences.";
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SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232
MEDLINE=21069356; PubMed=11197692;
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Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990)
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A BECODET-MORTEALE H.F.,

A BECODET-MORTEALE H.F.,

TOWNERTH: the methionine 196 arginine polymorphism in exon 6 of the

TYP receptor 2 gene (TNFRSF1B) is associated with the polycystic

CONTROLL SINGULAR H.F.,

COLIN. Endocrinol. Myetab. 87:3977-3987(2002).

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COLIN. Endocrinol. Suppressors BIRC3 and BIRC3 to TNFRSF1B/TNFR2. The TNF

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                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
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Peral B., San Millan J.L., Castello R., Moghetti
Escobar-Morreale H.F.;
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US2163; AACS0622.1; JOINED.
US2164; AACS0622.1; JOINED.
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US2160; AAC50622.1;
US2161; AAC50622.1;
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U52158; AAC50622.1;
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Q92956; Q8WXR1; Q96J31; Q9UM65;
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor (Herpesvirus entry mediator A) (Tumor necrosis factor-11ke 2)
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Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
"Herpes simplex virus-1 entry into cells mediated by a novel member of
the TNF/NGF receptor family.";
Cell 87:427-436(1996).
                                                                                                                                                                                                                                                                                23 LPAQVA----FTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDS
                                                                                                                                                                                                                                                     4 LPLQCVLWGCLLTAVHPEPPTACREKQYLINS--QCCSLCQPGQKLVSDCTEFTETECLP
                                                                                                                                                                                                                                                                                                                                        62 CGESEFLDTWNRETHCHQHKYCDPNLGLRVQ-----QKGTSETDTICTCEEGWHCT---
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MEDLINE=97306336; PubMed=9162061;
Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
Porter T.G., Truneh A., Young P.R.,
"A newly identified member of the tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     superfamily with a wide tissue distribution and involvement in
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Struyf F., Posavad C.M., Keyaerts E., Van Ranst M., Corey L.,
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Zhang W., Wan T., Cao X.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-21629477; PubMed=11756979;
                                                                                                                                                                                                             58;
                                                                                                                                                                   23.3%; Score 212.5; DB 1.
llarity 34.5%; Pred. No. 2.4e-12;
Conservative 12; Mismatches 58.
                                                                                                                                                                                                                                                                                                                                                                                                                          113 SEACESCVLHRSCSPGFGVKQIAVRPKT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 OEGCRLCAPLRKCRPGFGV----ARPGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte activation.";
J. Biol. Chem. 272:14272-14276(1997)
                 IISSUE=Cervical adenocarcinoma;
EMBL; BC052977; AAH52977.1;
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TISSUE=Skin;
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WEDLINE=22388257; PubMed=12477932;
A Grouse L.H., Derge J.G.,
A Idusher R.D., Collins F.S., Wagner L., Shemen C.R., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
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A Batchench C., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Brownstein M.J., McKernan K.J., Malek J.A., Gubaratne P.H.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Nilalon D.K., Maruy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
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A Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
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Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Chuman and mouse cDNA sequences.",
Brock. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-97298041; PubMed-9153189;
Hsu H., Solovyev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
"ATAR, a novel tumor necrosis factor receptor family member, signals through TRAF2 and TRAF5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWERTIVE Receptor for TNFSF14/LIGHT and homotrimeric TNFSF1/IMphotoxical and imphocyte activation. Plays an important role in HSV pathogenesis because it enhanced the entry of several wildtype HSV strains of both serotypes into CHO cells, and mediated HSV entry into activated human T cells.

-! SUBGNIT: Interacts with TRAF2, TRAF3 and TRAF2.

-! SUBCELIULAR LOCATION: Type I membrane protein (Probable).

-! TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION IN LUNG, SPLEEN, AND THYMUS.
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EMBL, AF373877; AAL47717.1; --
EMBL, AF373878; AAL47718.1; --
EMBL, BC002794; AAH02794.1; --
PDB, 1JMA; 26-SEP-01.
Genew; HGNC:11912; TNFRSF14.
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EMBL; U81232; AAD00505.1; -.
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Mol. Cell 8:169-179(2001).
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59 CLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHC---TSEA 115
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     GO; GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.
GO; GO:000505; P:cell surface receptor linked signal transdu. .; TAS.
GO; GO:0006955; P:cell surface receptor linked signal transdu. .; TAS.
InterPro; IPRO08063; Fas receptor.
InterPro; IPRO08063; Fas receptor.
Fam; PF00020; TNFR_c6; 3.
PRINTS; PRO0809; TNFR_C6; 3.
PRINTS; PRO0809; TNFR, 3.
PROSITE; PS000629; TNFR_NGFR_1; 1.
PROSITE; PS000629; TNFR_NGFR_2; 2.
Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism; SlGNAL
31 283 TUMOR_NECROSIS_FACTOR_RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 VLRLVLYLTFLGAPCYAPAL----PSCKEDEYPVGSECCPKCSPGYRVKEACGELTGTV
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N-LINKED (GLCNAC. ..) (POTENTIAL).
X -> R (in dbSNP:4870).
/FIId=VAR_01307.
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                                                                                                                  TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 283;
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                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TNFR-CYS 1.
TNFR-CYS 2.
TNFR-CYS 3.
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29.1%; Pred. No. 1.4e-11;
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/FTId=VAR_013440.
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Best Local Similarity 29.1.
Best Local 43; Conservative
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MARIANDER R., Marra M.A., Walley S., Marra M.A.;

MARIANDER R., Marra M.A., Marra M.A.;

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J. Biol. Chem. 275:14307-14315(2000).
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                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 3 precursor [Lymportoxin-beta receptor] (Tumor necrosis factor receptor)
ILTRO CARLO (Tumor necrosis factor C receptor).
ILTRO OR TURESF3 OR TNFCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P., Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid."; Genomics 16:214-218(1993).
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"A lymphotoxin-beta-specific receptor.";
Science 264:707-710(1994).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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J. Biol. Chem. 274:11868-11873(1999)
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MEDLINE=93252381; PubMed=8486360;
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                                             TNR3 HUMAN
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                                                                                                                                                                          MEDLINE-98172745; PubMed-9511754;
MEDLINE-98172745; PubMed-9511754;
Mizushina S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M., Otsuka M., Yamamoto T., Inoue J.-I., a clonding the human homolog of tumor necrosis factor receptor-associated factor 5 (TRAFS).";
Gene 207:135-140(1998).
I. FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTB, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3 and TRAFS. May play a role in the development of lymphoid organs.
I. SUBCELIULAR LOCATION: Type I membrane protein.
I. SUBCELIULAR LOCATION: Type I membrane protein.
                                                                                     MEDLINE-98289299; PubMed-9626059; Krajewska M., Krajewski S., Zapata J.M., VanArsdale T., Gascoyne R.D., Berern K., McFadden D., Shabaik A., Hugh J., Reynolds A., Clevenger C.V., Reed J.C.; "IRAF-4 expression in epithelial progenitor cells. Analysis in normal
                             "TKAF5, an activator of NF-kappaB and putative signal transducer for the lymphotoxin-beta receptor."; J. Biol. Chem. 271:14661-14664(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM, 600979; -...
GO, GO:0007165; P:signal transduction; TAS.
InterPro; IPR001864; Fas receptor.
InterPro; IPR001864; TARR c6.
Pfam; PR010020; TARR c6.
PRINTS; PR01680; PASRECEPTOR.
SMART; SM00208; TRRR, MSRR_1; 2.
PROSITE; PS00652; TNRR_NGFR_1; 2.
PROSITE; PS00650; TNRR_NGFR_2; 3.
Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
SIGNAL.
 MEDLINE-96278943; PubMed-8663299;
Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
Yagita H., Okumura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUPERFAMILY MEMBER 3. EXTRACELLULAR (POTENTIAL)
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TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 3.
TNFR-CYS 1.
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                                                                                                                                            adult, fetal, and tumor tissues.";
Am. J. Pathol. 152:1549-1561(1998)
[8]
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EMBL; BC026262; AAH26262.1;
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HSSP; P25942; 1CDF.
Genew; HGNC:6718; LTBR.
                                                                            INTERACTION WITH TRAF4.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the ENBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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- I. FUNCTION: Receptor for INFSF6/FASI. The adaptor molecule FADD

- I - FUNCTION: Receptor for TNFSF6/FASI. The adaptor molecule FADD

- recruits caspase-8 to the activated receptor. The resulting death-
inducing signaling complex (DISC) performs caspase-8 proteclytic

activation which initiates the subsequent cascade of caspases

(aspartate-specific oysteine proteases) mediating apoptosis. FAS-

mediated apoptosis may have a role in the induction of peripheral

tolerance, in the antigen-stimulated suicide of mature T-cells, or

both (By similarity).

- I- SUBUNIT: Binds DAXX and RIPKI (By similarity).

- SUBUNIT: Binds DAXX and RIPKI (By similarity).

- I- SUBUNIT: Binds DAXX and RIPKI (By similarity).

- I- SUBUNIT: SONTAINS A DAXTH DOWALN INVOLVED IN THE BINDING OF FADD,

AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.

- SIMILARITY: Contains 3 TNFR-Cys repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 FTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTS
                                                                                                                                                                                                                                                                                                                                                                                             16 PLVLGLFG-LLAASQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAKCSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                             58; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley, TISSUB=Liver,
MEDLINE=94120114, PubMed=7507668,
Minura K., Yamamoto M., Wakatsuki T.;
"A variant mRNA species encoding a truncated form of Fas antigen in the rat liver.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
40 N-LINKED (GLCNAC. ..) (POTENTIAL)
177 N-LINKED (GLCNAC. ..) (POTENTIAL)
46709 MW, 624626E6022F656F CRC64;
                                                                                                                                                               Length 435;
                                                                                                                                                                                                        Pred. No. 3.2e-11;
                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                             50; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 AA.
                                                                                                                                                                    21.9%; Score 200; 36.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 WALECTHCELLSDCPPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D26112; BAA05108.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 EA--CESCVLHRSCSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                          435 AA;
                                                                                                                                                                                                             Similarity
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 EPPTACREKQYLINSQCCSLCQPGQKLVSDC-TEFTETECLPCGE-SEFLDTWNRETHCH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
Pfam; PF00531; death; 1.

DR PRINTS; PR01680; FASTECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00206; TURF, 3.
DR PROSITE; PS00552; TURF, 12.
DR PROSITE; PS00552; TURF, NGFR_2; 2.
DR PROSITE; PS00507; TURF NGFR_2; 2.
DR PROSITE; PS0017; DEATH DOMAIN: Transmembrane; Repeat; Signal.
FT SIGNAL 22 324 TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY REBERTOR.
SUPERFAMILY RESERVED.

"""ANTIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY REBERTOR.
""""ANTIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR
""""ANTIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR
""""ANTIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR
""""ANTIN 22 324 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY REBERT 6.
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MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETDNNCSBGLYQVGPFCCQPCQPGGERKVKDCTTSGGAPTCHPCTBGEBYTDRKHYSDKCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .7e-10;
ss 69; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tunor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.6%; Score 188.5; DB 1; Length 324; 30.6%; Pred. No. 2.7e-10; ive 20; Mismatches 69; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D25D583C909D9D09 CRC64;
                                                                                                                                                                                                                                                   POTENTIAL.

TUPER-CYS 2.

TUPER-CYS 3.

DEATH.

BY SIMILARITY.

BY SIMILARITY.
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155 TRISNTKCKKQSSNYKLLMLLILP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 VRPKTWLCNRQAQT -- RLMLSVVP 157
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1189
1899
1899
1890
1891
1000
103
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DOMAIN
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DISULFID
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Suggs S., Boyle W.J.;

"Osteoprocegorin: a novel secreted protein involved in the regulation of bone density,";

"Cell 89:309-319(1997).

-!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclasts. Inhibits the activation of seems to depend on the local RANKL/OPG ratio, May also play a role in preventing arterial calcification. May act as decoy receptor in preventing acterial calcification. May act as decoy receptor in preventing acterial calcification. May also play a role in preventing acterial stopicials (By similarity).

-- SUBCELLULAR LOCATION: Secreted (By similarity).

-- INDUCTION: Upergulated by osteopontin.

-- INDUCTION: Opergulated by osteopontin.

-- SIMILARITY: Contains 2 death domains.
                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENELG utstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 HQHKYCDPNLG--LRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIMERIZATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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R HSSP; P25942; ICDF.

R InterPro; IPRO00488; Death.

R InterPro; IPRO00368; TNPR_c6.

R Ffan; PFC00020; TNRR_c6; 4.

R SMART; SM02009; TNRR; 4.

R RAST; SM02005; TNRR GF.

R PROSITE; PS50017; DEATH DOWAIN; FALSE_NEG.

R PROSITE; PS50017; DEATH DOWAIN; FALSE_NEG.

R PROSITE; PS50050; TNFR NGFR_1; 1.

R ROSITE; PS50050; TNFR NGFR_1; 1.

R Cytokine; Apoptosis; GIycoprotein; Repeat; Signal.

FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR

SUPERPAINITY MEMBER 11B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 181; DB.1; Length 401; ilarity 32.3%; Pred. No. 1.6e-09; Conservative 17; Mismatches 55; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEC6A31F1D4E573A CRC64;
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(GLCNAC. . .)
(GLCNAC. . .)
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BY SIMILARITY.
N-LINKED (GLCNAC. .
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TNFR-CYS 2.
TNFR-CYS 3.
TNFR-CYS 4.
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DEATH 2.
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41
65
83
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168
1088
401 AA,
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Best Local Similarity
Matches 42; Conserv
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SUGUENCE FROWN N., Shibata K., Yoshino M., Itoh M., Ishii Y., Katana-C57BL/61; TISSUB-Kidney;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arawai J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Arawa T., Hara A., Fukunishi Y., Konoo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casuvant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Okochiwa H., Kadoti T., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brach G., Burchien M.J., Bult C., Fletcher C., Fullia M., Gariboldi M., Lovonstein M.J., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Wilming L., Washima Y., Kawaji H., Kohtsuki S., Nashima Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH DAXX.
MEDLINE-97358633; PubMed=9215629;
Yang X., Khosravi-Far R., Chang H.Y., Baltimore D.;
"Daxx, a novel Fas-binding protein that activates JNK and apoptosis.";
[6] 89:1067-1076 (1997).
                                                                                         TURE MOUSE STANDARD; PRT; 327 AA.
P25446; Q9DCQ1;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-92148151; PubMed-1371136;
Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
Copeland N.G., Jenkins N.A., Nagata S.;
"The CDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.";
                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93189576; PubMed=7680478; Adachi M., Watchabe-Fukunaga R., Nagata S.; and transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr
                                                                                                                                                                                                                                                                                                                                                                                                                        Koczan D., Ibrahim S.M., Thiesen H.J.;
"Role of a mutant fas receptor in a transgenic mouse.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 148:1274-1279(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE OF 1-96 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:685-690(2001).
136 VRPKTWLCNR 145
                                                                                                                                                                                                TNFRSF6 OR APT1 OR FAS.
                          135 TPERNTVČKŘ 144
                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/Sv;
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RT antigen that mediates apoptosis.";

Antigen that mediates apoptosis.";

Rture 356:314-317(1992).

Rture 356:314-317(1992).

Rture 356:314-317(1992).

Inducting signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (asparate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).

CC :- SUBUNIT: Binds DAXX and RIPKI (By similarity).

CC :- SUBCHIT: Binds DAXX and RIPKI (By similarity).

CC :- SUBCHIT: Binds DAXX and RIPKI (By similarity).

CC :- SUBCHIT: Binds DAXX and RIPKI (By similarity).

CC :- SUBCHIT: Binds DAXX and RIPKI (By similarity).

CC :- SUBCHIT: DOMAIN: ADD ADUIT OWARY.

CC :- SUBCHIT: DOMAIN: ADD ADUIT OWARY.

CC :- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,

CC :- DISEASE: Defects in TNFRSF6 are the cause of the lymphadenopathy and autoantibody production.

CC :- SIMILARITY: Contains 3 TNFR-Cys repeats.

CC :- SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Procefford Agenth, Tenderdo, Inter-Co.
Pfam; PF00020; TNFR_co; 3.
PRINTS; PR01080; FASRECEPTOR.
SMART; SM00005; DEATH, 1.
SMART; SM00008; TNFR, 3.
PROSTIE; PS00062; TNFR NGFR 1; 2.
PROSTIE; PS00017; DEATH, DOWALN; 1.
PROSTIE; PS0017; DEATH, DOWALN; 1.
PROSTIE; PS0017; DEATH, DOWALN; 1.
PROSTIE; PS0017; DEATH, DOWALN; 1.
PROSTIC; PS0017; DEATH, DOWALN; 1.
MEDLINE=92195401; PubMed=1372394;
Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
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TWFR-CYS 3.
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EMBL; AK005590; BAB2211.1; -..
EMBL; AJ295702; CAC00638.1; JOINED.
EMBL; AJ295704; CAC00638.1; JOINED.
EMBL; S56496; AAB25700.1; JOINED.
EMBL; S56496; AAB25700.1; JOINED.
EMBL; S56496; AAB25700.1; JOINED.
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HSSP, P25445; IDDF.
MGD; MG195484; Trifrsf6.
InterPro; IPR000408; Death.
InterPro; IPR001368; TarF. Ge
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                                                       Nagata S.;
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"Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Lung cancer,
MEDLINE-98151033, PubMed-9492069,
WEDLINE-98151033, PubMed-9492069,
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
Tsuda B., Morinaga T., Higashio K.;
"Identity of osteoclastogenesis inhibitory factor (OCIF) and
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
                                                                                                                                                                                                                                    VHPEPPTACKEKQYLINSQCCSLCQPGQKLVSDCTEFTET-ECLPCGE-SEFLDTWNRET
                                                                                                                                                                                         68; Indels 14; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tilb HUMAN STANDARD, PRT, 401 AA.
000300, 060235, Q9UHP4;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
TNFRSF11B OR OPG OR OCIF.
                                                                          . .) (POTENTIAL) . .) (POTENTIAL)
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BEDLINE=295151659; PubMed=9688283;

MOTINGA T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;

"Cloning and characterization of the gene encoding human
                                                                                                                                                             Score 180; DB 1; Length 327;
Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor.";
                                                                                                    -> N (IN LPR).
-> R (IN REF. 3).
FGBFFC5ACE356EEE CRC64;
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
1 -> N (IN LER).
H -> R (IN REF. 3).
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37418 MW;
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327 AA;
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Best Local Similarity
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                DISULFID
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Ridausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A litschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A litschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
A litschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Human and mouse cDNA sequences."
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MEDITIME=21395914; PubMed=11505389;
Hofbauer L.C., Neubauer A., Heufelder A.E.;
Hoceptor activator of nuclear factor-kappaB ligand and osteoprotegerin: potential implications for the pathogenesis and treatment of malignant bone diseases.";
Cancer 92:460-470(201).
-!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98269100; PubMed=9603945; Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C., Dul E., Appelbauw E.R., Eichman C., DiPrinzio R., Dodds R.A., James I.E., Rosenberg M., Lee J.C., Young P.R.; "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL."; J. Biol. Chem. 273:14363-14367(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
MEDLINE=98148058; PubMed=3478964;
Yamaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
Morinaga T., Higashio K.;
"Characterization of structural domains of human osteoclastogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.; "Cloning and expression of osteoprotegerin from Homo sapiens."; Acta Biochim. Biophys. Sin. 31:680-684(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 22-36 AND 378-401.
MEDLINE-98238645; PubMed-9571159;
MEDLINE-98238645; PubMed-9571159;
Morinaga T., Tguda E., Higashio K.;
Morinaga T., Tguda E., Higashio K.;
"Characterization of monomeric and homodimeric forms of osteoclastogenesis inhibitory factor.";
Biochem. Biophys. Res. Commun. 245:382-387(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                         FROM N.A., AND VARIANT ASN-3.
Eur. J. Biochem. 254:685-691(1998).
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RESULT 13
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osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis.
                                                                                       -!- SUBCALT: Homodimer.
-!- SUBCALLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TASOUR SEPECTRICITY: Highly expressed in adult lung, heart, kidney,
liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
lymph node, trachea, adrenal gland, testis, and bone marrow.
Detected at very low levels in brain, placenta and skeletal
muscle. Highly expressed in fetal kidney, liver and lung.
-!- INDUCTION: Upregulated by increasing calcium-concentration in the
medium and estrogens. Downregulated by glucocorticoids.
-!- PTM: N-04-ycosylated. Contains sialic acid residues.
-!- PTM: The N-terminus is blocked.
-!- STMILARITY: Contains 4 TNFR-Cys repeats.
-!- SIMILARITY: Contains 2 death domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R GO; GO:0005125; F:Cytokine activity; TAS.
R GO; GO:0004872; F:Cytokine activity; TAS.
R GO; GO:000165; P:Signal transduction; TAS.
R GO; GO:0001501; P:Signal transduction; TAS.
R GO; GO:0001501; P:Skeletal development; TAS.
R InterPro; IPR001368; TNFR C6.
R Ffam; PF00020; TNFR C6; 3.
R SMART; SM00005; DEATH; 1.
R RSMART; SM00208; TNFR; 4.
R PROSITE; PS00052; TNFR; 4.
R PROSITE; PS00052; TNFR NGFR 1; 1.
R PROSITE; PS00052; TNFR NGFR 1; 1.
R PROSITE; PS00050; TNFR NGFR 1; 1.
R PROSITE; PS00050; TNFR NGFR 2; 2.
W Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
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TNFR-CYS 4.
DEATH 1.
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EMBL; AB002146; BAA25910.1; -.
EMBL; AB008822; BAA32076.1; -.
EMBL; AB008821; BAA32076.1; -.
EMBL; AB008821; BAA32076.1; -.
EMBL; AF134197; AAF20168.1; -.
HSSP; P25942; 1CPF.
Genew; HGNC:11909; TNFRSF11B.
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MIM; 602643;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 YCDPNLG--LRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIAVRPK 139
                                                                                                                                                                                                                                                                                                                                             81
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STRAIN=BALB/C; TISSUB=Kidney;
STRAIN=BALB/C; TISSUB=Kidney;
SIGNOTI: PubMed=9108485;
Signonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Suggs S., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Osteoprotegerin reverses osteoporosis by inhibiting endosteal osteoclasts and prevents vascular calcification by blocking a process resembling osteoclastogenesis.", J. Exp. Med. 192:463-474(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND ARG-296.
STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
MEDLINE=98382527; PubMed=9714833;
Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
Higashio K.;
                                                                                                                                                                                                                                                                                                                                          22 PPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHK
                                                                                                                                                                                                                                                                                                                                                                                              25 РРКУІНУВЕТЯНОІІСВКСРРСТУІКОНСТАКМКТУСАРСРВНУУТЬЯМНІЯВЕС---І
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "OSTEOprotegarin: a novel secreted protein involved in the regulation of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
AND ARG-296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteoclastogenesis inhibitory factor (OCIF) in embryogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tilb Mouse STANDARD; PRT; 401 AA.

008712; 070202;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin) (Osteoclastogenesis inhibitory factor)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                       .;
8
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                             MISSING: ABOLISHES DIMERIZATION.
D -> A (IN REF. 1).
EDF448B67D86C71E CRC64;
                                                                                                                                                                                                                    / Match 19.4%; Score 177; DB 1; Length 401; Local Similarity 31.0%; Pred. No. 3.7e-09; les 39; Conservative 16; Mismatches 63; Indels
                                 K -> N.
/FTId=VAR_013439.
C->S: ABOLISHES DIMERIZATION
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                                                                                                                                                                         46040 MW;
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gene and its expression
Gene 215:339-343(1998).
                                                                                    400
                                                                                                             400
263
401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 TWLCNR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 NTVCKR 144
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VARIANT
                                                                                                                MUTAGEN
CONFLICT
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                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                   Query Match
                                                                                    MUTAGEN
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TUFFACES 1.

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TUFFACES 4.

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DEATH 2.

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DEATH 4.

DEATH 5.

DEATH 7.

DEATH 7.

BY SIMILARITY.

BY SIMI
its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apports in vitro. Bane homeostasis seems to depend on the local RANKI,OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding blocks the inhibition of osteoclastogenesis. TRAIL binding -: SUBUNIT: Homodimer.
-: SUBUNIT: Homodimer.
-: TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta,
                                                                                                                                                                                              and in embryo.

--- DEVELOPMENTAL STACE: Detected in embryo at high levels on day 7, whereas expression decreases at day 11 and increases from day 15 to 17. On day 15 found in developing bone primordia, brachiocephalic artery and ductus arteriosus, left main bronchus, abdominal acrta and midgut.
--- INDUCTION: Upregulated by IGF-beta and estrogens. Downregulated by 1,25-dihdroxyvitamin D3 and parathyroid hormone.
--- SIMILARITY: Contains 2 death domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL).
SHISS).
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EMBL, AB013898; BAA28269.1; ---
EMBL, AB013903; BAA33388.1; JOINED.
EMBL, AB013900; BAA33388.1; JOINED.
EMBL, AB013901; BAA33388.1; JOINED.
EMBL, AB013902; BAA33388.1; JOINED.
EMBL, AB013902; BAA33388.1; JOINED.
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CARBOHYD
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P25119; P97893;
01-MAY-1992 (Rel. 22, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Las
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 HQHKYCDPNLG--LRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 IHYDPETG-----HOLLCDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDEC
                                                                                                                                                                                                                                                                                                                                                                                                18 VHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kissonerghis M., Fellowes R., Feldmann M., Chernajovsky Y., Submitted (MAY-1995) to the BMB/Cenbank/DBJ datebases. -!- FUNCTION: Receptor with high affinity for TRNSF2/TWF-alpha and approximately 5-fold lower affinity for homotrimeric TNRFST/Iymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRST1B/TWFR2 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91246168; PubMed=1645445; Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.; "Molecular cloniad expression of the type 1 and type 2 murine receptors for tumor necrosis factor."; Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
            N -> D (IN STRAINS 129/OLA AND NIH SWISS).
                                                                              S -- A (IN STRAINS 129/OLA AND NIH SWISS).
R (IN STRAINS 129/OLA AND NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91187885; PubMed=1849278; Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.; "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";
                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                             Length 401;
                                                                                                                                                                                                                                                                                                                                       57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jacob C.O., Liu J.,
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                R (IN STRAINS 129/OLA
                                                                                                                                                                                                                       CAA6102D3B312470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                   19.2%; Score 175; DB 1; 30.0%; Pred. No. 5.7e-09; ive 18; Mismatches 57;
                                                                                                                                                                                              SMISS)
                                                                                                                                                                                                                             401 AA; 45923 MW;
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                                                                                                                                                                                                                                                                                                                                             39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 VRPKTWLCNR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 TPERNTVČKK 144
                                                         165
                                                                                                                288
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                                                                                                             288
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                                                         165
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                                                                                                                                                                                                                                                                                         Query Match
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                                                         VARIANT
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      VARIANT
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AAA69407.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    smallpox virus genome.";
Nature 366:748-751(1993)
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                                                                                                                                                                                                                                                                                         protective mechanisms.
                                                                                           CRMB OR G2R OR G4R
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SEQUENCE FROM N.A.
                                                                                                                                              Orthopoxvirus.
NCBI_TaxID=10255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Esposito J.J.;
                                                          Soluble TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
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                                                                                                                                                                                                                         EMBL; W59378; AA440463.1; EMBL; W59378; AA440463.1; EMBL; U39488; AA450463.1; ---
EMBL; U39488; AAA85021.1; ---
EMBL; X87128; CAA6618.1; ---
BINE; B38634; B38634.
HSSP; P19438; INCF.
MGD; MGI:1314883; Thfrefib.
GO; GO:0001466; P:cell surface receptor linked signal transdu. . .; IMP.
GO; GO:0008220; P:noflammatory response; IMP.
GO; GO:0008220; P:noflammatory response; IMP.
InterPro; IPR001168; INFR_c6.
Emi; PF00200; INFR_c6; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 CNKTSDTVCADČEASMYTQVMNQFRTCLS---CSSSCTTDQVEIRACTKQQNRVCACEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRLPLQCVLWG-----CLLTAVHPEPPTACREKQYLIN---SQCCSLCQPGQXLVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Gaps
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TUTRE-CYS 2.

TUTRE-CYS 3.

TUTRE-CYS 4.

BY SIMILARITY.

BY SIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.9%; Score 173; DB 1; Length 474; llarity 28.6%; Pred. No. 1e-08; Conservative 21; Mismatches 64; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462EAE398C4D6563 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Repeat; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
SUBUNIT: Binds to TRAF2 (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 WHCT----SEACESCVLHRSCSPGFGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 RYCALKTHSGSCRQCMRLSKCGPGFGV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00652; TNFR NGFR 1; 2.
PROSITE; PS50050; TNFR NGFR 2; 3.
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CRMB_VARV
ID _CRMB_VARV STANDARD;
AC P34015; Q85407; Q89098; Q89118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50319 MW;
                                                                                                                                                                                                                EMBL; M60469; AAA39752.1; -.
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195
474 AA;
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les 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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SIGNAL
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DOMAIN
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349 AA.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelabb.eib.ch).
(Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last amnocation update)
receptor II precursor (cytokine response modifying protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Garcia-1966, and Somalia-1977;
Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M., Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=India-1967 / Isolate Indi;
MEDLINE=93202281; Pubmed=8384129;
Shchelkunov S.M., Sandakhchiev L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host
                                                                                                                                                                                                                           Variola virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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STRAIN-Garcia-1966;
MEDLINE-2010/299; PubMed=10639322;
MEDLINE-2010/299; PubMed=10639322;
Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter C.J.; "Potential virulence determinants in terminal regions of variola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R., Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N., Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
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Virology 266:361-386(2000).
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STRAIN-Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
Loparev V.N., Parsons J.M., Esposito J.J.;
Loparev Sequence as a criterion for allocation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         orthopoxviruses to a particular species.";
Submitted (JAN-1998) to the MBL/GenBank/DBU databases.
-!- FUNCTION: Receptor for INF-mediated antiviral processes (By the modification of INF-mediated antiviral processes (By
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-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.
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MEDLINE=94088747; PubMed=8264798;
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EMBL; U88146; P
EMBL; U88148; P
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A -> E (IN STRAIN SOWALIA-1977).
N -> D (IN STRAINS BUTLER-1952 AND GARCIA-1966).
P -> L (IN STRAINS BUTLER-1952 AND GARCIA-1966).
My D45D40B5C6E780BF CRC64;
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18.6%; Score 170; DB 1; Length 349;
Best Local Similarity 29.0%; Pred. No. 1.4e-08;
Matches 38; Conservative 21; Mismatches 64; Indels
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POTENTIAL.
SOLUBLE THE RECEPTOR II.
THER-CYS 1.
THER-CYS 2.
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EMBL; U88149; AAB94374.1;
EMBL; U88152; AAB94377.1;
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<sup>6</sup> LQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGES 65 8; Gaps g

<sup>66</sup> EFLDTWNRETHCHQ-HKYCDPNLGLRVQQKGTSET-DTICTCEEGWHCT---SEACESCV 120 72 IFTSRNHHLPACLSCNGRCNSN---QVETRSCNTTHNRICECSPGYYCLLKGSSGCRACV 128 ò g

<sup>121</sup> LHRSCSPGFGV 131

<sup>| |:||</sup> 129 SQTKCGIGYGV 139 à

Search completed: July 21, 2004, 10:05:59 Job time : 13 secs

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Q86yk5 homo sapien
Q86g34 sus scrofa
Q7yr15 canis famil
Q8wmq2 ovis aries
Q8kZx6 mus musculu
Q9jke0 rattus norv
Q9ddd2 gallus gall
Q9xs28 cercopithec
Q800k7 paralichthy
Q7z2y4 gallus gall
Q9r230 rattus norv
Q805b0 gallus gall
Q9r237 mus musculu
Q9c527 mus musculu
Q9bdp0 aotus trivi
                                                                                 July 21, 2004, 10:03:04; Search time 39 Seconds (without alignments) 1294.434 Million cell updates/sec
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1 MVRLELQCVLWGCLLTAVHP......WLCNRQAQTRLMLSVVPRIG 160
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Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_unclassified:*
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057110 variola vir 080513 variola vir 057108 monkeypox v 057271 monkeypox v 057101 morkeypox v 057101 morkeypox v 057101 morkeypox v 057101 morkeypox v 057108 camelpox vir 057128 camelpox vir 05710 morkeypox v 057100 morkeypox v 057301 morkeypox v 057301 morkeypox v 057201	Q9bopp macaca mula 05709 monkeypox v 088734 mus musculu Q861w6 felis silve Q96140 macaca mula 057109 variola vir 057097 camelpox vi
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## ALIGNMENTS

RESULT Q86YKS ID Q AC Q DT 0	TT 1 KS Q86YKS Q86YKS, 01-JUN-2003 01-JUN-2003	, , , ,	PRT; Created) Last sequ	; 223 AA. ed) sequence update)	
SEE	01-0CT-2003 (T)	rEMBLrel factor	Last anno or superf	. 25, Last annotation update) receptor superfamily member 5 (Fragment).	
88888888888888888888888888888888888888	INFKSF5. Homo sapiens (Human Bukaryota; Metazoa; Mammalia; Butheria;	sapiens (Human). yota; Metazoa; Chordata; lila; Eutheria; Primates;		Craniata; Vertebrata; Euteleostomi Catarrhini; Hominidae; Homo.	 .d
R RN	[1] SEOUENCE FROM N.A.	Z Z,			
RA	He X., Xu L.,	, Zeng Y , of CD40 isoform	in perip	heral mononuclear cells.";	
Z K	Submitted (JAN- EMBL: AY225405:	2003) AAO43	EMBL/GenB 	to the EMBL/GenBank/DDBJ databases. 1990.1:	
R.	GO; GO:0016020;	C:membrane;		400	
DR DR	GO; GO:0005743; GO; GO:0005488;	43; C:mitochondrial 88; F:binding; IEA.		inner membrane; ibA.	
H E			ane receptor	tor activity; IEA.	
Z Z		P:immune	•-		
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DR		IPR008063; Fas_rec	eptor.		
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Length 274; Indels

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61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
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Canis familiaris (Dog).
Canis familiaris (Dog).
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                     SEQUENCE FROM N.A.

Yang S., Sim G.-K.;

"Canine CD40 and CD40 Ligand cDNA Sequences.";

Submitted (JUL-2012) to the EMBL/GenBank/DDBJ databases.

EMBL, AY337989; AAP86653.1; -.

SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;
               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  Query Match 62.2%; Score 56%; DB 6; Le
Best Local Similarity 65.3%; Pred. No. 1.1e-56;
Matches 94; Conservative 18; Mismatches 32;
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01-OCT-2003 (TrEMBLrel.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                     ;
0
                                       Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                West K.A., Link. Rowden G.;
"Characterization of the Porcine CD40 Molecule.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF246845; AAL92924.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016988; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006915; P:immune response; IEA.
GO; GO:00165; P:signal transduction; IEA.
InterPro; IPR000035; Ras receptor.
InterPro; IPR000036; Ras receptor.
InterPro; IPR000036; TMFR GG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.4%; Score 615; DB 6; Length 270
Best Local Similarity 71.3%; Pred. No. 4.6e-62;
Matches 102; Conservative 14; Mismatches 27; Indels
                                       86.0%; Score 785; DB 4; Length 22 ilarity 95.1%; Pred. No. 1.3e-81; Conservative 1; Mismatches 6; Indels
 223
24659 MW; 85C63C20BC4E0B1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08SQ34;
01-UJN-2002 (TrEMBLrel. 21, Created)
01-UJN-2002 (TrEMBLrel. 21, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                    278 AA.
                                                                                                                                                                                                                         121 LHRSCSPGFGVKQIAVRPKTWLC 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO1680, FASRECEPTOR.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
 223 AA;
                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                  Matches 136;
 NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                    088034
                                                                                                                                                                                                                                                                         RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                     Q8WNQ2.
Q8WNQ2.
Q1-MRR-2002 (TrEMBirel. 20, Created)
Q1-MRR-2002 (TrEMBirel. 20, Last sequence update)
Q1-UNA-2003 (TrEMBirel. 24, Last annotation update)
Membrane protein CD40 (Fragment).
Membrane protein CD40 (Fragment).
Movis arises (Sheep).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AV072798; AAL68402.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane receptor activity; IEA.
GO; GO:0006915; P:immune response; IEA.
GO; GO:0000595; P:immune response; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR.c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;
121 MHSLCPPGLGVKQIATGISDTICD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM; PF00020; TNFR_c6; 4.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 4.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS00050; TNFR NGFR 1; 1.
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274 AA.

PRELIMINARY;

Q7YRL5 Q7YRL5;

Q7YRL5

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Q8K2X6

RESULT 5

Q8K2X6

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CD40 protein (Fragment).
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 62-169 FROM N.A.
STRAIN=Wister, TISSUES=Smooth muscle;
MEDLINE=99330195; PubMed=10403401;
MEDLINE=99330195; PubMed=10403401;
MEXZEEZ R., Wagner A.H., Cattaruzza M., Hecker M.;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer and EEBS Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG (GO:0005622) C:intracellular; IEA.
GG) GO:0016229; C:intracellular; IEA.
GG) GO:0016280; C:membrane; IEA.
GG) GO:0005840; C:ribosome; IEA.
GG) GO:0003735; F:structural constituent of ribosome; IEA.
GG) GO:0006915; F:structural constituent of ribosome; IEA.
GG) GO:0006915; P:sapoptcsis; IEA.
GG) GO:0006915; P:immune response; IEA.
GG) GO:0006415; P:protein biosynthesis; IEA.
GG) GO:0007465; P:signal transduction; IEA.
InterPro; IPR008063; Fas. receptor.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001865; Ribosomal_S2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Wistar; TISSUE=Smooth muscle;
Krzesz R., Hecker M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Smooth muscle;
Gao D., Hecker M.;
Submitted (MAR-201) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241231; AAF43717.2; ---
HSSP; Q92956; 1JMA.
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                                                                                                                                                   Last sequence update)
Last annotation update)
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PRINTS, PRO1680, FASRECEPTOR.
SMART, SMOGDOS0; TNFR; 3.
PROSITE; PS00962; RIBOSOMAL S2 1; 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 1; 1.
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                                                                                                   Created)
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                                                                                         01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity 53.1%
Local Similarity 53.1%
The second of the secon
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                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                               Q9JKEO;
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Q9DDD2
ID Q9DD1
SO THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT ST
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                                                                                                                                                                                                                                                       61 SCGKGEPLSTWNREKYCHEHRYCNPNLGLRIQSEGTLNTDTTCVCDEGQHCTSHTCESCT 120
                                                                                                                                                                                             PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
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                                                         MVRLPLOCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL 60
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to tumor necrosis factor receptor superfamily, member 5.
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Straubberg R.;

Straubberg R.;

Straubberg R.;

EMBL; BC029254; AMH29254.1;

EMBL; BC020254; AMH29254.1;

R GO; GO:0016020; Cimcmbrane; IEA.

GO; GO:0016020; Cimcmbrane; IEA.

GO; GO:0005631; Cimcleus; IEA.

GO; GO:0003677; F:DAA binding; IEA.

GO; GO:000377; F:DAA binding; IEA.

GO; GO:0006315; F:structural constituent of ribosome; IEA.

GO: GO:00
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54.2%; Pred. No. 2.9e-46;
cive 21; Mismatches 45; Indels
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Best Local Similarity 54.24
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
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                                                                                                             9
                                                                                                                                                          1 MIPIPOLCALWGCLLTAVHLGQCVTCSDKQYLQGGBCCDLCQPGNRLVSHCTALBKTQCQ 60
                                                                                                          1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                        Gaps
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0
     Length 169;
50.7%; Score 463; DB 11; Length 1.
53.1%; Pred. No. 6.5e-45;
iive 21; Mismatches 46; Indels
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RESULT

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9XSZB;
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGRIGILGILCALLIGCGQPGDAVNCSDKQYEHKGRCCNRCQPGKKLASECNDTEDSVCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PCENGGYQHSWTKERHCTPHEICEDNAGLIVKRHGNATHNTVCQCRAGMHCSDASCQTCV
                                                                                                                                     Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last amocation update)
Tumor necrosis factor receptor superfamily member 14 precursor.
                                                                                                                                                                                                                                                                                                           Tregaskes C.A.;
Theshs (2001), University of Reading, Reading, UNITED KINGDOM
EMBL; AJ737100; CAC20218.1; -
HSSP; Q92956; LJMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
32.4%; Score 296; DB 13; Length 276;
Best Local Similarity 37.7%; Pred. No. 1.3e-25;
Matches 49; Conservative 25; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Thymus;
STRAIN=C57BL/6; TISSUE=Thymus;
Benencia F., Conejo-dercia J.R., Courreges M.C., Coukos G.;
"Light regulation in a murine model of ovarian carcinoma.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AYSC4405; AA0089081.1; -.
GO; GO:0016020; C:membrane; IE.
GO; GO:0016020; C:membrane; IE.
                                                                                                                                                                                                                                                                                                                                                                                                GO, GO:0016020; C:membrane; IEA.
GO; GO:001604; C:nucleus; IEA.
GO; GO:0005644; C:nucleus; IEA.
GO; GO:0005648; F:RNA binding; IEA.
GO; GO:0006915; P:tansmembrane receptor activity; IEA.
GO; GO:0006915; P:tamune response; IEA.
GO; GO:0007165; P:tamune response; IEA.
InterPro; IFR008065; Fas receptor.
InterPro; IFR008065; Ras receptor.
InterPro; IFR001005; Myb_DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00037; MYB 1; 1.
PROSITE; PS00623; TMF NGFR 1; 1.
PROSITE; PS500503; TMF NGFR 2; 3.
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;
                                             Last sequence update)
Last annotation update)
                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00020; TNFR c6; 3.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-OCT-2003 (TrEMBLrel. 25,
Q9DDD2;
01-MAR-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 LHRSCSPGFG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ENEPCKQGFG 130
                                                                                          Human CD40-homologue.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q80WM9
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Q80WM9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 TAHANGLSKCLPCGVCDPDMGLLTWQECSSWKDTVCRCIPGYFCENQDGSHCSTCLQHTT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 LDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSE---ACESCVLHRS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Kidney,
MEDLINE=99296730; PubMed=10366573;
MEDLINE=99296730; PubMed=10366573;
Foster T.P., Chouljenko V.N., Kousoulas K.G.;
Frunctional characterization of the HveA homolog specified by African green monkey kidney cells with a herpes simplex virus expressing the green fluorescence protein.";
Virology 258:365-374(1999)
EMBL; AF147720; AAD37381.1;
HSSP; Q92956; LUMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 CVFLINLLQRISAQP--SCRQEBFLVGDECCPMCNPGYHVKQVCSEHTGTVCAPCPPQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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GO: GO:0004888; F:transmembrane receptor activity; IEA.
GO:0006915; P:apoptosis; IEA.
GO:0006955; P:immune response; IEA.
GO:00006955; P:signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                Potential.
C4A7EAD8EFC0521D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0652; TNFR_NGFR_1; 1.
PROSITE; PSS0050; TNFR_NGFR_2; 2.
SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62;
                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 25.1%; Score 229.5; DB 1 Local Similarity 30.9%; Pred. No. 5.4e-18; hes 43; Conservative 29; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 AA.
GO, GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Pas receptor.
InterPro; IPR001368; INFR_c6.
Pfam; PR00020; TNFR_c6; 4.
SMRNT; SM00208; TNFR, 4.
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                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 CSPGFGVKQIAVRPKTWLC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 CPPGQRVEKRGTHDQDTVC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 275 AA; 30171 MW;
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PRINTS, PR01680, FASRECEPTOR.
SMART, SM00208, TNFR, 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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NON TER
SEQUENCE
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 CDSGQYMEKANYAQKCLSCUKCKSNKGLQYAQRCSSTTRTGCVCKPGMYCIMDFDNPYCA 124
                                                           SCKEDBYPVGSECCPKCGPGFHVRQACGEQTGTVCEPCSPGTYIAHFNGLSKCLQCQMCD 100
                                           85 PNIGLRVQQKGTSETDTICTCEEGWHC---TSEACESCVLHRSCSPGFGVKQLAVRPKTW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACREKQYLINSQCCSLCQPGQKLVSDCTEPTETECLPCGESEFLDTWNRETHCHQHKYCD 84
                                                                                                                                                                                                                                                                                                                                        Park C., Kurobe T., Hirono I., Aoki T.; "Cloning and characterization of cDNAs for two distinct tumor necrosis factor receptor superfamily genes from Japanese flounder Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LPLQCVLWGCLLTAVHPEPPTACREK - QYLINSQCCSLCQPGQKLVSDCTEFTETECLP
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                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectoidei; Paralichthyidae; Paralichthys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.5%; Score 196.5; DB 13; Length 30.6%; Pred. No. 5.7e-14; ive 19; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                           olivaceus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 AA; 52227 MW; EE55874A8C7F2085 CRC64;
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Last annotation update)
                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                  Paralichthys olivaceus (Flounder)
                                                                                                                                                                                                                            Tumor necrosis factor receptor-2.
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les 41; Conservative
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                                                                                                                                                                     PRELIMINARY;
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Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                       142
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                                                                                                                                               RESULT 10
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78 HQHKYCDPNLG--LRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 LHYDPGTS---RQVM-----CNQCPPGSYVKQHCTAASPTVCAPCPDQYYAEDWNSNDEC
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Wistar; TISSUE=Corpus luteum;
Lareu R.R., Dharmarajan A.;
"Cloning and expression of Fas and Fas Ligand in the apoptotic rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 146;
                                                                                                                                                                                                                   Bridgham J.T., Johnson A.L.;
Bridgham J.T., Johnson A.L.;
Bridgham J.T., Johnson A.L.;
Bridgham J.T., Johnson A.L.;
Costeoprortogerin (OPG) expression in the hen ovary.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY251407; AAP03690.1;
COSTON AND ARD3690.1;
COSTON AND ARD369.1 F. Receptor activity; IEA.
InterPro; IPRO0620; EGF like.
InterPro; IPRO01368; TNFR C6.
Pfam; PF00020; TNFR C6; 3.
SNRAT; SN00208; TNFR; 3.
SNRAT; SN00208; TNFR; 3.
PROSITE; PS01652; TNFR NGFR 1; 1.
PROSITE; PS00509; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0006202; C:membrane; IEA.
GO; GO:0006488; F:transmembrane receptor activity; IEA.
GO; GO:00064915; P:sapoprosis; IEA.
GO; GO:00065915; P:immune response; IEA.
GO; GO:000165; P:immune response; IEA.
GO; GO:0001165; P:signal transduction; IEA.
InterPro; IPR008063; Faa receptor.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; INFR_GC.
Pfam; PF00100; TNPR_GC; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SMO0208; TNFR, 2.
PROSITE; PS00652; TNFR_NGFR_1; 1.
PROSITE; PS00652; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Indels
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EMBL; AF104034; AAD20221.1; -- HSSP; Q92956; LJMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16487 MW; 1C9E64FE3A0FC2DF CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.5%
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                                                                                   Gallus.
NCBL_TaxID=9031;
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INFRSF1B.
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Q9BDP0;
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                                                                                       21 EPPTACREKOYLINSQCCSLCQPGQXLVSDC-TEFTETECLPCGE-SEFLDTWNRETHCH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 PPTACREKOYLINSOCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHK 81
                                                                                                         34 ETDNNCSEGLYQVGPFCCQPGERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.

STRAIN=White leghorn H-B15; TISSUE=Spleen;
STRAIN=White leghorn H-B15; TISSUE=Spleen;
Syde A., Horuchi H., Furuseaw S., Marsuda H.;
Molecular clouchi H., Furuseaw S., Marsuda H.;
Molecular cloning and characterization of chicken Tumor necrosis
factor receptor-II (TNFR-II) and Tumor necrosis factor receptor
II associated factor-5 (TRAF-5) genes.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
II Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AB10.1004; BAC55966.1; E.

R GO; GO:0004888; Firansmembrane receptor activity; IEA.
GO; GO:0004888; Firansmembrane response; IEA.
GO; GO:0004888; Firansmembrane response; IEA.
GO; GO:0004888; Firansmembrane response; IEA.
GO; GO:0007165; Psignal transduction; IEA.
GO; GO:0007165; Psignal transduction; IEA.
FIREPRO; IPRO00308; TNFR.c6; J.
FRINT: PRO0020; TNFR.c6; J.
FRANT: SMART; SMO0208; TNFR. 4.
FROMETE; PSO00652; TNFR. 4.
FROMETE; PSO00652; TNFR. MGFR.1; 2.
FRANT: PROSITE; PSO00652; TNFR. MGFR.2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 YCDP--NLGLRVQQKGTSETDTICTCEEGWHCTS---EACESCVLHRSCSPGFGVKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -CSPPCRKGFVENQTCTLSWDRICSCPPNEYCISKMYQNCHICKVHKKCGRGYRVSR 144
                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.3%; Score 176.5; DB 13; Length 462; 30.8%; Pred. No. 1e-11; live 16; Mismatches 54; Indels 11;
                                                                                                                                                          79 OHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSC 125
                                    19.7%; Score 180; DB 11; Length 150; 33.6%; Pred. No. 1.3e-12; tive. 14; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sayde A.A.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
150 150
150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;
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                                                                                                                                                                                                                                                 Q805B0;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=White leghorn H-B15; TISSUE=Spleen;
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                      Numor necrosis factor receptor-II.
                                                              Conservative
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                                                  Best Local Similarity
Matches 36, Conserv
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RESULT 14

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61 PCGESEFLDTWNRETHCHQHKYCDPNLGL-RVQQKG-TSETDTICTCEEGWHCT----SE 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1314883; Thfrsflb.

GO; GO:000594; P:nflamatory response; IMP.

GO; GO:0006954; P:inflamatory response; IMP.

GO; GO:0008220; P:necrosis; IMP.

InterPro; IPR001368; TNFR_c6.

Pfam; PF00120; TNFR_c6; 4.

PROMIT: PR001208; TNFR_12.

PROSITE; PS50050; TNFR_MGFR_1; 2.

PROSITE; PS50050; TNFR_NGFR_2; 3.
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                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mush.TaxID=10090;
                                                                                                                                                                                                                                                                                  STRAIN=NDD;
Powell B.E., Wicker L.S., Peterson L.B., Todd J.A.;
Amino acid variation in the tumor Necrosis factor receptor 2 is
linked to autoimmune diabetes in NOD mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Powell B.E., Wicker L.S., Peterson L.B., Todd J.A.; "Allelic variation of the type 2 tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 459;
             062327;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-NOV-2003 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
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93 T -> I.

268 F -> I.

421 Y -> C.

48686 MW, 6C51D2CF1C4626DF CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 SCROCMRLSKCGPGFGV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mamm. Genome 5:726-727(1994).
EMBL; 1X76401; CAA53981.1; -.
PIR; 1X48854; 148854.
HSSP; P19438; 1NCF.
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(TrEMBLrel. 17, I
(TrEMBLrel. 25, I
PRELIMINARY;
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93
268
345
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93
268
268
345
421
459 AA;
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01-JUN-2001
01-OCT-2003
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WE TOURNOTE FROM N.A.

WE TOURNOTE FROM N.A.

WE SEQUENCE FROM N.A.

WE SEQUENCE FROM N.A.

WE WELLINE=21383618; PubMed=11491535;

WE WILLINGER F., Bostik P., Mayne A.E., King C.L., Genain C.P.,

We wiss W.R., Ansari A.A.;

We wiss W.R., Ansari A.A.;

The Cloning, sequencing, and homology analysis of nonhuman primate

The Tas/Fas-ligand and co-stimulatory molecules.";

I mmunogenetics 53:315-328(2001).

RE Fas/Fas-ligand and co-stimulatory molecules.";

RESP: P25445; IDDF.

RESP: P25445; IDDF.

RESP: P25445; IDDF.

RESP: P25445; IDDF.

ROG: 000006205; Firansmembrane receptor activity; IEA.

ROG: 000006315; P:aspoptosis; IEA.

ROG: 000006315; P:aspoptosis; IEA.

ROG: 000006315; P:signal transduction; IEA.

ROG: 000000515; P:signal transduction; IEA.

ROG: 00000165; P:signal transduction; IEA.

ROG: 00000166; P:signal transduction; IEA.

ROG: 00000
Aotus trivirgatus (Night monkey) (Douroucouli).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=9505;
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18.7%; Score 170.5; DB 6; Length 328;
Best Local Similarity 32.4%; Pred. No. 3.66-11;
Matches 36; Conservative 18; Mismatches 54; Indels 3;
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Search completed: July 21, 2004, 10:06:50 Job time: 40 secs

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86 NIGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIAV 136

3; Gaps

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The present sequence is human CD40. It may be used in a method for preventing latent virus reactivation or controlling virus replication. The method comprises administering a composition capable of binding to a cell membrane expressed CD40, where the binding of the composition to the CD40 on the surface of the cell generates a stimulatory signal to the cell. The method is useful for treating immunocompromised patients, e.g. infected with human immunodeficiency virus (HIV), or immunosuppressed patients, e.g. of due to infections or illness, or as a side effect of treatments (such as radiation or cancer therapy), or due to tissue or organ transplantation. The method does not have the levels of toxicity seen following administration of conventional antiviral drugs
                                                                                                                                                                                                                                                                                                            Method for preventing latent virus reactivation or controlling virus replication by administration of antibodies or similar reagents which stimulate the CD40 molecule.
                                                                                                                                                                                              (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 18; 36pp; English.
                                                                                                                                                                                                                                   Sarawar SR, Schoenberger SP;
                                                                                                                  28-APR-2000; 2000WO-US011734
                                                                                                                                                      99US-0131730P
                                                                                                                                                                                                                                                                           WPI; 2001-024740/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 277 AA;
                                     WO200066155-A1.
    Homo sapiens
                                                                                                                                                        30-APR-1999;
                                                                             09-NOV-2000
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ö PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120 PCGESBFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSBTDTICTCBBGWHCTSBACESCV 120 9 9 1 MVRLPLOCVLWGCLLTAVHPEPPTACREKOYLINSOCCSLCOPGOKLVSDCTEFTETECL MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL Gaps . 0 DB 4; Length 277; Score 785; DB 4; Length 27 Pred. No. 4e-58; 1; Mismatches 6; Indels LHRSCSPGFGVKQIAVRPKTWLC 143 LHRSCSPGFGVKQIATGVSDTIC 143 86.0%; 95.1%; Query Match 86.0 Best Local Similarity 95.1 Matches 136; Conservative 121 61 61 121 셤 g ò 셤 8 ò

AAB50520 standard; protein; 277 AA. (first entry) 15-MAR-2001 AAB50520; RESULT 15 AABSOSZO
XX
AC AABS
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DT 15-P
XX
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DX HUME
XX
XW HUME
XW TUMM
XW TUMM
XW TUMM
XW GAP
XW GAP
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XX
XX
HOM
XW GAP
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XX
HOM

Human tumour necrosis factor receptor CD40 protein SEQ ID NO:10.

Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nootropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptocis inducing ligand; vasotropic; immunosuppressive; neuroprorective; antiviral; antiinflammatcory, anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.

sapiens Ношо

WO200071150-A1.

30-NOV-2000.

2000WO-US013515 18-MAY-2000; 20-MAY-1999;

(HUMA-) HUMAN GENOME SCI INC.

<u>ن</u> Gentz RL, Ruben SM, Wei Y,

WPI; 2001-041051/05.

Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.

Disclosure; Fig 2; 285pp; English.

The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor entracellular domain, also referred to as tumour necrosis factor receptor of (TNFR-5 or TRE)). TRID has cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral, antinflammatory, anticonvulsant, nootropic, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasorropic activities, and can be used in gene therapy. The TRID polymucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after etimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polymucleotides, proteins, antibodies, and anticasses and anticasses are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) cuseful in the diagnosis, treatment or prevention of: (a) cancer; (b) cutofinders; (c) diseases ascolated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention

Sequence 277 AA;

Gaps Score 785; DB 4; Length 277; Pred. No. 4e-58; 1; Mismatches 6; Indels 86.0%; Best Local Similarity Matches 136; Conservative Query Match Best Local Similarity

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61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120 61 ò d

LHRSCSPGFGVKQIATGVSDTIC 143 LHRSCSPGFGVKQIAVRPKTWLC 121 à

Search completed: July 21, 2004, 10:05:36

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LHRSCSPGFGVKQIAVRPKTWLC 143
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                                                                                                                                                                                                                                                                                                          25-OCT-2000; 2000WO-US041532.
                                                                                                                                                                                                                                                                                                                                                         99US-01612B1P
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Best Local Similarity 95.1%;
Matches 136; Conservative
  03-AUG-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-308629/32.
                                                 Human CD40 antigen
                                                                                                                                                                                                                                                                                                                                                                                                         (TANO-) TANOX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutically
                                                                                                                                                                                                                WO200130974-A2.
                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999;
                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AAB37807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the expression of a target nucleic acid (tNA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a compounds with the tNA sequence. The method comprises generating a cavaluating in silico the binding of the virtual compounds with the tNA according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of a tNA sequence via binding of the ONS that modulate the expression of a tNA sequence via binding of the ONS with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and (2) a method of defining a set of compounds that modulate the expression of a tNA sequence via binding of compounds that modulate the expression of a tNA sequence via binding of compounds that the that. The methods can be used for the generation and identification of synthetic compounds having defined physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences that are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. Addition of Additional Additional Additional Additional Additional A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying compounds which modulate expression of nucleic acids, used to provide compounds having defined physical, chemical or bioactive properties, e.g. antisense activity.
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                                                                                                                                                                                                                                                                                                                                                         Brooks
nucleotide sequence-based technology; antisense drug discovery.
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Pred. No. 4e-58;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                       Sasmor HM,
                                                                                                                                                                                                                                                                                                                                                       Freier SM,
Vickers TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 177-179; 264pp; English.
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                                                                                                                                                                                                                                                                                                                                                       F, Mcneil J,
Borchers AH,
                                                                                                                                                                                                                                    98US-0081483P.
98US-00067638.
                                                                                                                                                                                        99WO-US008268.
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Best Local Similarity 95.1%;
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                         BF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-620446/53.
N-PSDB; AAZ40936.
                                                                                                                                                                                                                                                                                                                                                                                Wyatt JR,
                                                                                                                                                                                                                                                                                                                                                         Baker
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                                                 Homo sapiens
                                                                                              WO9953101-A1
                                                                                                                                                                                        13-APR-1999;
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28-APR-1998;
                                                                                                                                           21-OCT-1999
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Novel CD40-binding non-antibody molecule, that do not cause proliferation, differentiation or activation of CD40-expressing cells but which inhibit CD40 ligand-induced activation, used to treat autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to non-antibody molecules which bind to an epitope on CD40 antigan and do not activate CD40-expressing cells, but inhibit CD40-ligand (CD40L) induced activation, and which do not interfere with the binding of CD40L to CD40. The present sequence is human CD40 antigen. CD40 is a 50 kDA type 1 membrane glycoprotein expressed on a variety of cells, including B cells. CD40 is critical for B cell function. The non-antibody molecules of the present invention are useful for treating autoimmune, cell-mediated and antibody-mediated diseases, and conditions in which immunogenic proteins are used
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human immunodeficiency virus; HIV; cancer; organ transplantation.
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Pred. No. 4e-58;
1; Mismatches 6; Indels
Human; CD40; immunosuppressive; B cell; autoimmune disease; cell-mediated disease; antibody-mediated disease.
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AAB84892

RESULT 13 AAB84892 ID AAB84 XX AC AAB84

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This invention describes novel pure proapoptotic dependence peptides dependence of an active dependence domain selected from dependence bolypeptides consisting of p75NTR, androgen receptor, DCZ, huntingtin polypeptide, Machado-Joseph disease gene product, SCA1, SCA2, SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of inducing cell death and can be used to develop products to mediate or inhibit apoptosis. The methods can be used for reducing the severity of proapoptotic dependence domain mediated pathological conditions e.g. Spinocerebellar ataxias, dentacroubzopallidoluysian atrophy, Machado-Joseph disease, stroke or head trauma. They can also be used for reducing proliferation or cell survival e.g. neoplastic, malignant, autoimmune or fibrotic conditions. This sequence represents the human CD40 polypeptide
Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke; dentatorubropallidoluysian atrophy; cell proliferation; cell survival; neoplastic; malignant; autoimmune; fibrotic; CD40.
                                                                                                                                                                                                                                                                                                                          New proapoptotic dependence peptides, used to develop products for treating, e.g. Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 170-171; 199pp; English.
                                                                                                                                                           99WO-US005250.
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136; Conservative
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                                                                                                                                                                                                                      (BURN-) BURNHAM INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 276 AA;
                                                                                                                                                           11-MAR-1999;
                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to substantially pure CD40 splice variant proteins which include tail sequences. Also disclosed is a pharmaceutical composition comprising the protein and a carrier, an in vitro method of detecting whether an individual is expressing the protein, and a method for modulating CD40-CD154 interactions in an individual. The protein of the invention is useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury. The current sequence represents CD40 splice variant protein.
                                                                                                                                                                                                                                                                                                                                                                                            Protein, useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury.
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huntingtin polypeptide, Machado-Joseph disease, SCA1, SCA2, SCA6;
atrophin-1; cell death, apoptosis, Huntington's disease; head trauma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
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Pred. No. 3.6e-58;
1; Mismatches 6; Indels
                                                   #SEQ ID
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95.1%;
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                                                 CD40 splice variant protein
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Best Local Similarity 95.1
Matches 136; Conservative
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                                                                                                                                                                                                                                                                                     (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-697601/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 244 AA;
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                     20-NOV-2003
                                                                                  CD40; splice
                                                                                                 nflammatory
                                                                                                                                Homo sapiens
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PCGESEFLDTWNRETHCHOHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
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                                                                                                                                                                                                     Gaps
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                                                                                                                             86.0%; Score 785; DB 2; Length 276; 95.1%; Pred. No. 4e-58; ive 1; Mismatches 6; Indels
described in the method of the invention
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121 LHRSCSPGFGVKQIATGVSDTIC 143
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                                                                                   ADA25634;
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                                    RESULT 9
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                                                 ADA25634
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                                                 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                  CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic; inflammatory disease; cancer; atherosclerosis; acute injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PCGESEFLDTWARETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to substantially pure CD40 splice variant proteins which include tail sequences. Also disclosed is a pharmaceutical composition comprising the protein and a carrier, an in vitro method of detecting whether an individual is expressing the protein, and a method for modulating CD40-CD154 interactions in an individual. The protein of the invention is useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury. The current sequence represents CD40 splice variant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein, useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease,
1 WYRLPLQCVIWGCLLTAVHPBPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                    PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDT1CTCEEGWHCTSEACESCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 785; DB 6; Length 22:
Pred. No. 3.3e-58;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, atherosclerosis or acute injury.
                                                                                                                                                                                                                                            CD40 splice variant protein #SEQ ID 8.
                                                                                  121 LHRSCSPGFGVKQIAVRPKTWLC 143
                                                                                                         121 LHRSCSPGFGVKQIATGVSDTIC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHRSCSPGFGVKQIAVRPKTWLC 143
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                                                                                                                                                                     ADA25636 standard; protein; 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.0%;
95.1%;
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                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity your Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                           (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-697601/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                              WO2003070768-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bernstein J,
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Best Local (
                                                                                                                                              RESULT 8
ADA25636
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PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
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                                                                                                                                                                                                                                                                 CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to substantially pure CD40 splice variant proteins which include tail sequences. Also disclosed is a pharmaceutical composition comprising the protein and a carrier, an in vitro method of detecting whether an individual is expressing the protein, and a method for modulating CD40-CD154 interactions in an individual. The protein of the invention is useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury. The current sequence represents CD40 splice variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein, useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury.
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                                                                                                                                                                                                                                                                                                    inflammatory disease; cancer; atherosclerosis; acute injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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95.1%; Pred. No. 3.46-58;
                                                                                                                                                                                                 CD40 splice variant protein #SEQ ID 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 82-83; 92pp; English.
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ADA25634 standard; protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-FEB-2003; 2003WO-IB000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2002; 2002US-0358877P
                                                                                                                              (first entry)
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nes 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bernstein J, Mintz L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003070768-A2.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; wild-type; extracellular domain; CD40-6XHis.
                                                                  PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                             61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                       1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
               MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                                                                                                                             Human CD40-6XHis wild-type extracellular domain protein.
                                                                                                                           121 LHRSCSPGFGVKQIAVRPKTWLC 143
                                                                                                                                                  LHRSCSPGFGVKQIATGVSDTIC
                                                                                                                                                                                                                            ADE28516 standard; protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2002; 2002WO-US036107.
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                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PFIZ ) PFIZER PROD (ABGE-) ABGENIX INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003040170-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                  29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                       ADE28516;
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ADE2851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant; antiinflammatory, cytostatic; antiarteriosclerotic; disease; cancer; atherosclerosis; acute injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to substantially pure CD40 splice variant proteins which include tail sequences. Also disclosed is a pharmaceutical composition comprising the protein and a carrier, an in vitro method of detecting whether an individual is expressing the protein, and a method for modulating CD40-CD154 interactions in an individual. The protein of the invention is useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury. The current sequence represents CD40 splice variant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein, useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury.
therapy procedures. The current sequence is that of the human CD40 (D1-D3)-6XHis mutant extracellular domain protein of the invention.
                                                                                                                                            MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                   PCGESEFLDTWNRETHCHOHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV
                                                                                                                                                                                   PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDT1CTCEEGWHCTSEACESCV
                                                                                                                           1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                Gaps
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llarity 95.1%; Pred. No. 2.8e-58;
Conservative 1; Mismatches 6; Indels
                                                                  Score 785; DB 7; Length 153;
Pred. No. 2.2e-58;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                         LHRSCSPGFGVKQIAVRPKTWLC 143
                                                                                                                                                                                                                                                                    121 LHRSCSPGFGVKQIATGVSDTIC 143
                                                                                                                                                                                                                                                                                                                                        ADA25632 standard; protein; 191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 79-80; 92pp; English
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                                                                   86.0%;
95.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-2002; 2002US-0358877P
                                                                                                                                                                                                                                                                                                                                                                                                                             CD40 splice variant protein
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                   Ouery Match
Best Local Similarity 95.1
Matches 136; Conservative
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                                          Sequence 153 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD40; splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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Best Local Simi
Matches 136;
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                                                                                                                                                              New chimeric or human monoclonal antibody or its antigen-binding portion that specifically binds to and activates human CD40, useful for enhancing an immune response in a human, or treating cancer, HIV, neutropenia or viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 86.0%; Score 785; DB 7; Length 197; Best Local Similarity 95.1%; Pred. No. 2.9e-58; Matches 136; Conservative 1; Mismatches 6; Indels
Feng
Jia X,
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 14; SEQ ID NO 139; 177pp; English.
Corvalan J,
                                                                                        WPI; 2003-441521/41.
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                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metabolic research; oxifan; agonist; antagonist; body mass; obesity; hyperlipidaemia; atheroscalexosis; insulin resistence; diabetes; hypertension; anorectic; antilipemic; antiarteriosclerotic; antidiabetic; hypotensive; immunomodulator; anti-HIV; gene therapy.
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a CD40R variant and affecting the binding affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to agonists and antagonists of oxifan, a member of the tumour necrosis factor receptor superfamily. These can be
                                                                                                                                                                                                                                                                                                                                                                              61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV
                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV
                                                                                                                                                                                                                                                              1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                                                                                                                                    1 MVRLPLÓCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LHRSCSPGFGVKQIAVRPKTW-------LCNRQAQTRLMLSVVPRI 159
                                                                                                                                                                                                       13;
                                                                                                                                                 Length 246;
                                                                                                                                                                                                    Indels
                                                                                                                                        Score 787.5; DB 4;
Pred. No. 2.2e-58;
5; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .20
label= signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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|label=_EC_domain
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/label= IC domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABR63594 standard; protein; 246
capable of binding to a CD40R valof the variant to a CD40 ligand
                                                                                                                                              86.3%;
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N-PSDB; ACC85399.
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                                                                                          Sequence 246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR63594;
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                                                                                                                                                                                                                                                               61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                              PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-CD40 monoclonal antibody, CD40; cytostatic; virucide, antibacterial; immunostimulant; anti-HIV; hyperproliferative; cancer; viral; bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy; human; mutent; mutein; excracellular domain; (D1-D3)-6XHis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y portion
enhancing
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used in preventing and treating obesity-related diseases, including hyperlipidaemia, atherosclerosis, insulin resistance, diabetes and hypertension. The present sequence is the human oxifan protein described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chimeric or human monoclonal antibody or its antigen-binding portic
that specifically binds to and activates human CD40, useful for enhanci
an immune response in a human, or treating cancer, HIV, neutropenia or
                                                                                                                                                                                             1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                                                                                  WYRLPLOCYLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                                                                                                                                              Gaps
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                                                                                                                            Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human CD40 (D1-D3)-6XHis mutant extracellular domain protein.
                                                                                                                                                                                                                                                                                                                                     LHRSCSPGFGVKQIAVRPKTW-------LCNRQAQTRLMLSVVPRI
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                                                                                                                        Score 787.5; DB 6;
Pred. No. 2.2e-58;
5; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 14; SEQ ID NO 140; 177pp; English.
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                                                                                                                        86.3%;
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Best Local Similarity 83.0
Matches 142; Conservative
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                                                                                         Sequence 246 AA;
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Sequence 156 AA;

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e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple sclerosis, inflammatory diseases and graft versus host disease. Also claimed are methods for detecting the presence of a variant CD40R in a sample, for determining the level of variant CD40R in a sample, and for determining the ratio between the level of a CD40R variant acid and the level of criginal CD40R, and a method for identifying candidate compounds capable of binding to a CD40R variant and afficity of the variant to a CD40R ligand
                                                                                                                                                                                                                                                                                                                                                             PCGESEFIDIWNRETHCHOHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                        61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD40, splice variant, antiinflammatory, cytostatic, antiarteriosclerotic, inflammatory disease, cancer, atherosclerosis, acute injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to substantially pure CD40 splice variant proteins which include tail sequences. Also disclosed is a pharmaceutical composition comprising the protein and a carrier, an in vitro method of detecting whether an individual is expressing the protein, and a method for modulating CD40-CD154 interactions in an individual. The protein of the invention is useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury. The current sequence represents CD40 splice variant protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein, useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury.
                                                                                                                                                                                                                                                                                 1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQXLVSDCTEFTETECL
                                                                                                                                                                                                                                                                                                             MYRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTECL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHRSCSPGFGVKQIAVRPKTWLCNRQAQTRLMLSVVPRIG 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD40 splice variant protein #SEQ ID 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1, Page 83-84; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA25635 standard; protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eshel D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COMP-) COMPUGEN LTD
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The present sequence is that of a novel splice variant of the human CD40 receptor (CD40R). The variant has the extracellular domain of the native protein from the signal peptide up to the amino acid before the transmembrane region. 6 Novel splice variants (see AAB20169-74) of human and murine CD40R, nucleic acids (see AAB30275-80) encoding them, and murine CD40R, nucleic acids (see AAB30275-80) encoding them, and murine CD40R, nucleic acids (see AAB30275-80) encoding them, as a pharmaceutical composition consisting of a variant CD40R polypeptide is a pharmaceutical composition consisting of a variant CD40R polypeptide for treatment of diseases which can be ameliorated, cured or prevented by increasing the level of a CD40R variant; antibodies can be used to reduce the level of a CD40R variant; antibodies can be used to reduce the level of a CD40R variant; antibodies can be used to reduce the level of a CD40R variant of lugus erythematosus, and multiple sclerosis, inflammatory diseases and graft versus host disease. Also claimed are methods for determining the presence of a variant CD40R in a sample, and for determining the ratio between the level of a CD40R variant acid and the level of original CD40R, and a method for identifying candidate compounds
                                          0
                                                                                                                                                              61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                               61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding alternative splicing variant of CD40 receptor, useful for treating inflammatory diseases, autoimmune diseases, and graft versus host reaction.
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                                                                                                               1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTBFTETECL
                                                                                 1 MVRLPLQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECL
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD40 receptor; CD40R; human; splice variant; antiinflammatory; immunosuppressive; antiarthritic; antirheumatic; dermatological; neuroprotective; therapy; diagnosis.
                                          ö
  Length 156;
                                          0; Indels
                                                                                                                                                                                                                                                                 121 LHRSCSPGFGVKQIAVRPKTWLCNRQAQTRLMLSVV 156
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97.6%; Score 891; DB 6; I
100.0%; Pred. No. 2.8e-67;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD40 receptor splice variant.
                                                                                                                                                                                                                                                                                                                                                                                       AAB20170 standard; protein; 246 AA
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                       Similarity
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Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1586107 segs, 282547505 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

Description	20169 Humar	25635 CD40 s	20170 Humar	335	28517 Humar	5632 CD40	28516 Huma	36 CD40	25634 CD40	5630	3499 Huma	2701 Human	1892 Human	78	0520 Human	Aae19354 Human CD4	Aao18051 CD40 B-ce	8	00	3061 Humar	52 CD40 w	1920 Human	27 Human	122	Ada09880 Human rec
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ADE25748 AAR38859 AAY32191	ABG22935 ABP70128 ADA49703	AAY94713 AAY95322 ADE28518	AAY58212 ADA25638 ABG22934	AAB20171 AAY58213 AAB20173	AAB66982 AAB20172 AAY94715 AAB20174 AAW94647
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22,72	306 125 163	163 278 111	274 160 839	156 195	197 203 203 211 75
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22 6 27 6	0 6 6 6 6 6 6 6 6 6 6 6	8 8 8 8 8 8	35 37	38 39 40	4 4 4 4 4 4 6 6 4 8

### ALIGNMENTS

AABSOLT 1 10 AAB 20169 XXX AAB 20169 XXX AAB 20169 XXX AAB 30- XXX AAB 30- XXX HOM WO 25- XXX WO 25
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	ption	80 Mouse CD4	78 Mouse CD4	99 Mouse CD4	79 Mouse CD4	77 Mouse CD4	00 Mouse CD4	51 CD40 wild	17 CD40 cDNA	06 Human CD4	54 Human CD4	Human	Human	32 Human CD4	90 Human cel	69 Human CD4	.84 Human lym	CD40 E	89 Human sig	Human	89 Human Mox	93 Human CD4	21 Human dis	51 Farnesvl
	Description	Aaf30280	Aaf30278	Abd744	Aaf30279	Aaf3027	Abq74500	Ada 25651	Aan9061	Aat14706	Aav63454	Aaz40936	Aav81198	Aaz2343	Aaa50590	Aaz47769	Aas03184	Aa147328	Aca56689	Acc72771	Acc00289	Abx1459	Add18921	Ade85051
SUMMAKIES	ID	AAF30280	AAF30278	ABQ74499	AAF30279	AAF30277	ABQ74500	ADA25651	AAN90617	AAT14706	AAV63454	AAZ40936	AAV81198	AAZ23432	AAA50590	AAZ47769	AAS03184	AAL47328	ACA56689	ACC72771	ACC00289	ABX14593	ADD18921	ADE85051
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Ade25641 Human CDA Aaq71176 Human CDA Aaq4741 CD40 Cod1 Aaz20296 CD40 COD1 Abye9405 Human NOV Acc85599 Human OX1 Aaf30276 Human OX1 Ada09918 Human CD4 Ada25631 CD40 spli Ada25633 CD40 spli Ada25633 CD40 spli Ada25633 CD40 spli Ada25537 CD40 spli Aas87122 DNA encod Aaz5528 Canine CD Aaz5528 Canine CD Aaz5528 Canine CD Aaz5528 Canine CD Aaz5530 Canine CD Aaz55530 Canine CD Aaz55530 Canine CD Aaz55530 Canine CD Aaz55530 Canine ma Aaz55537 Canine CD Aaz55537 Canine CD Abv99404 Human NOV Aaz55539 Canine CD Aaz55539 Canine CD Aaz55539 Canine CD Aaz55539 Canine CD	SLNE		cDNA clone Mcd40Alt6Corecte.	ariant; antiinflammatory; irheumatic; dermatological; sis; ss.						e splicing variant of CD40 receptor, diseases, autoimmune diseases, and graft	cDNA encoding splice e mouse CD40 receptor	acids of the original CD40R ctor receptor (TNFR) Cys repe 4, with 30 alternative C-term
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amino acids. In addition, there is a 9-amino acid insert at position 86 of the original protein, instead of the original Asn. The variant is missing part of TNRR Cys repeat 4, the transmembrane domain and the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of human and murine CD40R, nucleic acids (see AAF30275-80) encoding them, expression vectors, host cells and anti-CD40R antibodies are claimed. Also claimed is a pharmaceutical composition consisting of an expression vector comprising a CD40R nucleic acid, for treatment of diseases which can be ameliorated, cured or prevented by either decreasing the level or of at least 1 ligand of CD40R, by increasing the level of a CD40R variant, or by reducing the level of a CD40R variant. The diseases in challed autoimmune diseases e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple sclerosis, inflammatory diseases and graft versus host disease. Also claimed are methods for detecting the presence of a variant nucleic acid sequence of CD40R in a sample, for determining the level of variant nucleic acid sequences of CD40R in a sample, and for determining the level of the original CD40R, e.g. using a nucleic acid chip ö 180 420 480 480 540 540 099 120 TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCTCTTGAGAAGACCCAATGCCAC 180 CCATGTGACTCAGGCGAATTCTCAGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCAC 240 CCATGTGACTCAGGCGAATTCTCAGGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCAC 240 AGACACTGTGAACCCAGTGCGTGGGGCTGCCTGGGAAGGGATCAAGGGCTTCGGGTTAAG 300 420 600 600 660 GGGCAGTGTTTACGTGCAGTGACAACAGTACCTCCACGATGGCCAGTGCTGTGTTTTG 120 241 AGACACTGTGAACCCAGTGCGTGGGCTGCCTGGGAAGGGGATCAAGGGCTTCGGGTTAAG 300 9 TGCCAGCCAGGCAAGCCGACTGAAGCCACTGCACAGCTCTTGAGAAGACCCAATGCCAC 1 ATGGTGTCTTTGCCTCGGCTGTGCGCGCTATGGGGCTGCTTGTTGACAGCGGTCCATCTA CTATATCAAAAAGGTGGTCAAGAACCAAAGGATAATGAGATGTTACCCCCTGCGGCTCG CTATATCAAAAAGGTGGTCAAGAAACCAAAGGATAATGAGATGTTACCCCCTGCGGCTCG GGGCAGTGTGTTACGTGCAGTGACAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG 361 AGCAAGGATTGCGAGGCATGTGCTCAGCACGCCCTGTATCCCTGGCTTTGGAGTTATG AGCAAGGATTGCGAGGCATGTGCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCG GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTTCTCC 421 GAGATGGCCACTGAGGCCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTTCTCC AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCG 541 AGCCCTGCTGGTCATTCCTGTCGTGATGGGCATCCTCATCACCATTTTCGGGGTGTTTCT AGCCCTGCTGGTCATTCCTGTCGTGATGGGCATCCTCATCACCATTTTCGGGGTGTTTCT Gaps ·; 100.0%; Score 809; DB 4; Length 809; .larity 100.0%; Pred. No. 4e-249; Conservative 0; Mismatches 0; Indels Sequence 809 BP; 194 A; 213 C; 229 G; 173 T; 0 U; 0 Other; 1 ATGGTGTCTTTGCCT Local Similarity les 809; Conserv 61 121 121 181 181 241 301 361 421 481 481 541 109 109 661 Query Match Best Loca Matches g ò d ŏ g ò g ò g ઠે g g g g à g ð 엄  $\delta$ 8 ò

The present sequence is that of mouse cDNA encoding splice variant McdAAlt8 (see AAB20172) of the mouse CD40 receptor (CD40R). The variant contains 165 N-terminal amino acids of the original CD40R sequence including tumour necrosis factor receptor (TNFR) Cys repeats 1, 2 and 3, acids I.t is missing part of TNFR repeat 4, the transmembrane domain and the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of human and murine CD40R, nucleic acids (see AAF30275-80) encoding them, expression vectors, host cells and anti-CD40R antibodies are claimed. Also claimed is a pharmaceutical composition consisting of an expression vector comprising a CD40R nucleic acid, for treatment of diseases which can be ameliotrated, cured or prevented by either decreasing the level or of at least 1 ligand of CD40R, by increasing the level of a CD40R variant, or by reducing the level of a CD40R variant. The diseases include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus include autoimmune diseases e.g. rheumatoid arthritis, systemic lupus erythematosus, and multiple sclerosis, inflammatory diseases and graft versus host disease. Also claimed are methods for detecting the presence of cavinat nucleic acid sequence of CD40R in a sample, for determining the level of the original CD40R, e.g. using a nucleic acid chip 721 GGAGACACTGCACGGGTGTCAGCCTGTCACAGGAGGAGGATGGTAAAGAGAGTCGCATCTC 780 Nucleic acid encoding alternative splicing variant of CD40 receptor, useful for treating inflammatory diseases, autoimmune diseases, and graft GGAGACACTGCACGGGTGTCAGCCTGTCACACAGGAGGATGGTAAAGAGAGTCGCATCTC 780 CD40 receptor; CD40R; mouse; splice variant; antiinflammatory; immunosuppressive; antiarthritic; antirheumatic; dermatological; neuroprotective; gene therapy; diagnosis; ss. Sequence 776 BP; 188 A; 206 C; 213 G; 169 T; 0 U; 0 Other; Mouse CD40 receptor splice variant cDNA clone Mcd40Alt8. AGTGCAGGAGCGGCAGGTGACAGACAGCA Location/Qualifiers Elazar M; Claim 1; Page 59-60; 70pp; English. AAF30278 standard; cDNA; 776 BP. 19-JUL-2000; 2000WO-IL000427. (first entry) Savitzky K, Khosravi R, versus host reaction. (COMP-) COMPUGEN LTD WPI; 2001-147341/15. P-PSDB; AAB20172. WO200105967-A1. 20-JUL-1999; 25-JAN-2001. 30-APR-2001 781 781 AAF30278; Mus q ઠે d 661 ACGGCAAGATCCCCAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTGCA 720 ACGGCAAGATCCCCAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTGCA

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Mouse; DNA array sequence selection; gene; cDNA microarray; probe;

Mouse CD40 nucleotide sequence SEQ ID NO:17.

21-OCT-2002

ABQ74499

ВP

ABQ74499 standard; cDNA; 1579

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probes that are immobilised on a solid support, where the array comprises at least 10-20 probes having sequences selected from the 29 sequences of 192-4655 base pairs given in ABC7481 to ABC74511. Also described is a method for selecting DNA sequences for a non-redundant microarray, comprising: (a) providing sequence databases; (b) screening the databases specific for a species and a tissue found in the sequences specific for a species and a tissue found in the sequences from the list to generate a non-redundant cluster list; (d) categorising selected sequences from non-redundant cluster list; (d) categorising selected sequences from non-redundant cluster list; (d) based on the characteristics used to establish the parameters of the module list. The composition comprising the microarrays is useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a composition comprising an array of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising an array of cDNA probes immobilized on a support, useful for diagnostic and screening procedures involving immunologically-based sample materials, drug testing or monitoring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 679; DB 6; Length 1579;
Pred. No. 3.5e-207;
0; Mismatches 0; Indels 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1579 BP; 391 A; 379 C; 428 G; 381 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 3; 420pp; English.
                                                                                                                                                                                                                   19-DEC-2001; 2001WO-US050618.
                                                                                                                                                                                                                                                               19-DEC-2000; 2000US-00741238
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Best Local Similarity 90.1%;
Matches 785; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-608530/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease progression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD40 receptor; CD40R; mouse; splice variant; antiinflammatory; immunosuppressive; antiarthritic; antirheumatic; dermatological; neuroprotective; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse CD40 receptor splice variant cDNA clone Mcd40Alt19.
                                                                                                                                              AATCAGTCATCACTTTTCGAAAGTGTTATCCCTGGACAA----
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 249 AGACACTGTGAACCCA-
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The present sequence is that of mouse CDNA encoding splice variant

CC contains 16S N-terminal amino acids of the original CD40R sequence

CC contains 16S N-terminal amino acids of the original CD40R sequence

including tumour necrosis factor receptor (TNRR) Cys repeats 1, 2 and 3,

cc acids. It is missing part of TNRR repeat 4, the transmembrane domain and

CC acids. It is missing part of TNRR repeat 4, the transmembrane domain and

CC acids. It is missing part of TNRR repeat 4, the transmembrane domain and

CC the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of

the cytoplasmic domain. 6 Novel splice variants (see AAB20169-74) of

Novel splice variants of the consisting of an expression vector comprising a CD40R nucleic acid, for treatment of diseases which

CC an be ameliorated, cured or prevented by either decreasing the level or

CC can be ameliorated, cured or prevented by either decreasing the level or

CC fat least 1 ligand of CD40R, by increasing the level of a CD40R

CC variant, or by reducing the level of a CD40R variant. The diseases

CC include autoimmune diseases e.g. rheumatoid arrhitis, systemic lupus

CC variant, or by reducing the level of a CD40R variant. The diseases

CC include autoimmune diseases e.g. rheumatoid arrhitis; systemic lupus

CC variant nucleic acid sequences of CD40R in a sample, for determining

CD the level of variant nucleic acid sequences of CD40R in a sample, and for

CC and the level of the original CD40R, e.g. using a nucleic acid chip
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                                                                                            Nucleic acid encoding alternative splicing variant of CD40 receptor, useful for treating inflammatory diseases, autoimmune diseases, and graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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67.6%; Score 547; DB 4; I
Best Local Similarity 95.3%; Pred. No. 6.7e-165;
Matches 584; Conservative 0; Mismatches 5;
Elazar M;
                                                                                                                                                                                Claim 1; Page 60; 70pp; English.
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Savitzky K, Khosravi
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P-PSDB; AAB20173.
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DFB1-1-5 (see AAB20171) of the mouse CD40 receptor (CD40R). The variant

contains 135 N-terminal antho acids of the original sequence including

tumour necrosis factor receptor (TDRE) Cys repeats 1 and 2, and part of

missing the TNFR repeat 4, part of repeat 3, the transmembrane domain and

the cytoplasmic domain. 6 Novel splice variants (see AAB20165-74) of

human and murine CD40R, mucleic acids (see AAB202165-74) of

human and murine CD40R, mucleic acids (see AAB202165-74) of

human and murine CD40R, mucleic acids (see AAB202165-74) of

human accounting composition consisting of an expression vector.

comprising a CD40R nucleic acid, for treatment of diseases which can be

ameliorated, cured or prevented by either decreasing the level or of at

last 1 ligand of CD40R, by increasing the level of a CD40R variant, or

by reducing the level of a CD40R variant. The diseases include autoimmune

cultiple sclenosis, inflammatory diseases and graft versus host disease.

Also claimed are methods for detecting the presence of a variant nucleic

acid sequence of CD40R in a sample, for determining the level of variant

nucleic acid sequences of CD40R variant nucleic acid and the level of

ratio between the level of a CD40R variant nucleic acid and the level of

the original CD40R, e.g. using a nucleic acid chip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding alternative splicing variant of CD40 receptor, useful for treating inflammatory diseases, autoimmune diseases, and graft versus host reaction.
AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAAGTCCCGGATGCG 516
                          AGCCCTGCTGGTCATTCCTGTCGTGATGGGCATCCTCATCACCATTTTCGGGGGTGTTTCT 600
                                                   517 AGCCCTGCTGGTCATTCCTGTGTGATGGGCATCCTCATCACCGTTTTCGGGGTGTTTCC 576
                                                                                                                                                                                                                                                                                       CD40 receptor; CD40R; mouse; splice variant; antiinflammatory; immunosuppressive; antiarthritic; antirheumatic; dermatological; neuroprotective; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                             receptor splice variant cDNA clone Mcd40-pFB1-1-5.
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
33. .503
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Elazar M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 59; 70pp; English.
                                                                                                                                                                            AAF30277 standard; cDNA; 934 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-2000; 2000WO-IL000427.
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                                                                                CTATATCAAAAG 613
                                                                                                     CTATATCAGIGAG 589
                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Savitzky K, Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COMP-) COMPUGEN LTD
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P-PSDB; AAB20171.
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                                                                                                                                                                                                       GGGCAGTGTGTTACGTGCAGTGACAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG
                                                                                                                                                                                                                                               93 GGGCAGTGTGTTACGTGCAGTGACAAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG
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                                                                                                                         1 AIGGIGICITIGCCICGGCIGIGCGCGCIAIGGGGGCIGCTIGITGACAGCGGICCAICIA
                                                                               Gaps
                                                                               26;
                                   Length 934;
Sequence 934 BP; 246 A; 218 C; 231 G; 226 T; 0 U; 13 Other;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse CD40 image clone nucleotide sequence SEQ ID NO:18.
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                                   Score 429.2; DB 4;
Pred. No. 5.5e-127;
0; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ74500 standard; cDNA; 469 BP
                                     Query Match
Best Local Similarity 84.5%;
Matches '541; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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CD40; splice variant; antiinflammatory; cytostatic; antiarteriosclerotic; inflammatory disease; cancer; atherosclerosis; acute injury; gene; ds.

CD40 wild-type protein encoding DNA #SEQ ID 23

20-NOV-2003 (first entry)

ADA25651;

/\*tag= a /product= "CD40 wild-type protein"

/\*tag=

WO2003070768-A2

28-AUG-2003

Location/Qualifiers 48. .881

Homo sapiens

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The present invention describes a composition comprising an array of cDNA probes that are immobilised on a solid support, where the array comprises at least 10-20 probes having sequences selected from the 29 sequences of 12-4655 base pairs given in ABC/4483 to ABC/4511. Also described is a method for selecting DNA sequences for a non-redundant microarray, comprising; (a) providing sequence databases; (b) screening the databases of pecies to generate a redundant sequence list; (c) removing redundant sequences from the list to generate a non-redundant cluster list; (d) categorising selected sequences from non-redundant cluster list into at least one module list; and (e) selecting the best representative clones based on the characteristics used to establish the parameters of the module list. The composition comprising the microarrays is useful in diagnostic and screening procedures involving immunologically-based sample materials. It is used in experiments and screens in innate and
                                                                                                                                                                                                                                                       New composition comprising an array of cDNA probes immobilized on a solid support, useful for diagnostic and screening procedures involving immunologically-based sample materials, drug testing or monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adaptive basic immunology, tumour immunology, cancer biology of immune cells, aging, drug testing, infection immunology, autoimmune diseases, arthritis, allergy, and vaccine development against these diseases. The composition and method may be used in monitoring the progression of particular disease, in screening drug treatments for diseases, and in the construction of non-redundant DNA microarrays for different species
                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 3; 420pp; English.
19-DEC-2001; 2001WO-US050618
                                                   19-DEC-2000; 2000US-00741238
                                                                                                                                                                                                                                                                                                                                   disease progression.
                                                                                                                                                                                                         WPI; 2002-608530/65
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TTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCGAGCCCTGCTGGTC TITICGAAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCGAGCCCTGCTGGTC 554 ATTCCTGTCGTGATGGGCATCCTCATCACCATTTTCGGGGGTGTTTCTCTATATCAAAAG 61 ATTCCTGTCGTGATGGGCATCCTCATCACCATTTTCGGGGTGTTTCTCTTATATCAAAAG GTGGTCAAGAAACCAAAGGATAATGAGATGTTACCCCCTGCGGCTCGACGGCAAGATCCC CAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTGCAGGAGACACTGCAC 181 CAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCCAGTGCAGGAGACGCTGCAC GGGTGTCAGCCTGTCACACACAGGAGGATGGTAAAGAGAGTCGCATCTCAGTGCAGGAGCGG 121 Gregicaagaaaccaaaggaraargagarcrraccccrgcggcrcgacggaagarccc Gaps ; 38.7%; Score 312.8; DB 6; Length 469; 99.4%; Pred. No. 1e-89; 1ve 0; Mismatches 2; Indels 0 Sequence 469 BP; 110 A; 120 C; 136 G; 103 T; 0 U; 0 Other; CAGGTGACAGAGCA 316 CAGGTGACAGACAGCA 809 Conservative Best Local Similarity Matches 314; Conserv 494 614 674 734 301 Query Match ò g ò g à g 8 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to substantially pure CD40 splice variant proteins which include tail sequences. Also disclosed is a pharmaceutical composition comprising the protein and a carrier, an in vitro method of detecting whether an individual is expressing the protein, and a method for modulating CD40-CD154 interactions in an individual. The protein of the invention is useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating confosition for modulating CD40-disease, cancer, atherosclerosis or acute injury. The current sequence represents CD40 wild-type protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein, useful for preparing a composition for modulating CD40-CD154 interactions in an individual for treating chronic inflammatory disease, cancer, atherosclerosis or acute injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GGGCAGTGTGTGTGCGCGGTGCAAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%; Score 280.4; DB 8; 62.7%; Pred. No. 3.7e-79; rative 0; Mismatches 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 90; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  Eshel D;
                                                                                                                                                                                                                                                                                                                                         22-FEB-2002; 2002US-0358877P.
                                                                                                                                                                                                                                                                                                            24-FEB-2003; 2003WO-IB000665
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                                                                                                                                                                                                                                                                                                                                                                      (COMP-) COMPUGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-697601/66.
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Best Local &
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AAATACTGCGACCCCA-------AACTAGGGCTTCGGGTCCAG 323

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RESULT 7 ADA25651 ID ADA25651 standard; DNA; 910 BP.

cell

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Gaps

107 120 167 227

287 300 323 360 420 443 480 503 527 563 623

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CD40 encodes a cell surface antigen involved in cell mediated immunity. This DNA can be expressed in a vector which transforms COS cells. The vector can isolate any protein, and clones are easy to manipulate. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCTCTTGAGAAGACCCAATGCCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAAGGGCACCTCAGAAACAGACACCCATCTGCACCTGTGAAGAAGGCTGGCACTGTACG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccrrecegraaaeceaarrccraaaccreaaaaaaaacacacacaccaccaccac
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    - Accechagasanter recedada de la contra del la c
                                                                                                                                                                                                                                                                                                                                                                   1 ATGGTGTCTTTGCCTCGGCTGTGCGCGCTATGGGGGCTGCTTGTTGACAGCGGTCCATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGACGGCAAGATCCCCAGGAGATGGAAGATTATCCCGGGTCATAACACACCGCTGCTCCAGTG
                                                                                                                                                                                                                                                                                                                              89;
                                                                                                                                                                                                                                                                                     Score 280.4; DB 1; Length 1004;
Pred. No. 3.9e-79;
0; Mismatches 231; Indels 89;
                                    encoding
                                                                                                                                                                                                                                                  Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;
                                    Rapid immuno:selection cloning - used to clone genes enco
surface antigens associated with mammalian T lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 17; 69pp; English
                                                                                                                                                                                                                                                                                   34.7%;
                                                                                                                                                                                                                                                                                                          Local Similarity 62.7
hes 538; Conservative
WPI; 1989-250302/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A cDNA clone. (AAT14714) codes for human cell surface antigen CD40. It was isolated using a rapid immunoselection method in which a cDNA library is constructed in mammalian (e.g. COS) cells using novel expression vectors (see also AAT14702 and AAT14705), and cells expressing the antigen are selected using antibody-coated plates (panning). This immunoselection cloning method, developed to clone genes for cell surface antigens of human lymphocytes (see also AAT14703-04 and AAT14706-26), has general appli. Cell surface antigens are obtd. for diagnostic and therapeutic use. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGGCAGTGTTACGTGCAGTGACAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG 120
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  801 CAGGAGACTTTACATGGATGCCAACCGGTCACCAGGAGGATGGCAAAGAGAGTCGCATC 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aregirceicrecercies anecencies de consecue de consecuencies de 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning of cDNA encoding cell surface antigen - useful for isolation of diagnostic and therapeutic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell surface antigen; cloning; immunoselection; immunotherapy; therapy; diagnosis; vector; CD40; CO5; lymphocyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGTGTCTTTGCCTCGGCTGTGCGCGCTATGGGGCTGCTTGTTGACAGCGGTCCATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 280.4; DB 2; Length
Pred. No. 3.9e-79;
0; Mismatches 231; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Fig 16; 79pp; English.
                                                                                                                                                                                                                  AAT14706 standard; cDNA; 1004 BP
                                                TCAGTGCAGGAGCGCAG 796
                                                                                                rcagracagadadada 878
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89US-00379076.
90US-00553759.
92US-00983647.
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62.7%;
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                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 62.77
Matches 538, Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Human CD40 antigen cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-200279/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1988;
13-JUL-1989;
13-JUL-1990;
01-DEC-1992;
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                                                                                                                                                                                                                                                                                                             25-MAR-2003
30-OCT-1996
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ID AAT14706

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860

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A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tNA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA
   624 AGAGCCCTGGTGGTGATCCCCATCATCTTCGGGATCCTGTTTGCCATCCTCTTGGTGCTG 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compounds which modulate expression of nucleic acids, used provide compounds having defined physical, chemical or bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 GTTGTGCAACAGGCAGACACAACAAGACTGATGTCTGTGGTCCCCAGGATCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     659 CGACGGCAAGATCCCCAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGAGACACTGCACGGGTCAGCCTGTCACACAGGAGGATGGTAAAGAGAGTCGCATC
                                                                                                                                                                                                                                                                                                                                                           599 CICIAIAICAAAAAGGIGGICAAAAAACCAAAGGAIAAIGAGAIGITACCCCCIGCGGCI
                                                                                                                                                                                                                                                                                                                                                                                                                     Grettrareaaaageresecaasaasecaaceaaraassececececececeaseas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ACCCCAGGAGATCAATTTTCCCGACGATCTTCCTGGCTCCAACACACTGCTGCTCCAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence-based technology; antisense drug discovery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sasmor HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Freier SM,
Vickers TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 177-179; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     properties, e.g. antisense activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker BF, Mcneil J,
tt JR, Borchers AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ40936 standard; cDNA; 1004 BP
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98US-00067638.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CD40 encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-620446/53
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28-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nucleotide sequence comprises human CD40 antigen cDNA. It was isolated by a novel method for cloning cDNAs from mammalian expression clibraries that is based on transient expression of an antigen in cukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate, such as a culture dish. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a cukaryotic cell. It has been used to clone games (see AAV63442-c3).

CC encoding cell surface antigens from mammalian lymphocytes (see AAV6344.

CC 55). The isolated genes can be expressed in a prokaryotic or eukaryotic chost cells to produce the encoded protein. The invention also provides (clipt efficiency expression vectors (see AAV63441 and AAV63444) which allow the generation of very large mammalian expression libraries. The purified genes and proteins are useful for immunodianneric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purified genes and proteins are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders of animals, including humans. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                               New cloning vector and poly:linker - based on existing sequences fireficient cloning and expression of mammalian cDNA(s), especially lymphocyte antigenic sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;
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90US-00498809.
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                                                                                                                          (GEHO ) GEN HOSPITAL CORP
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es 538; Conservative
                                                                                                                                                                                                                                                        WPI; 1998-609251/51
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                           13-JUL-1990;
01-DEC-1992;
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according to defined criteria. Also described are: (1) a method of defining a set of oligomucleotides (ONs) that modulate the expression of a LNA sequence via binding of the ONs with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONs with the tNA according to defined criteria, and (2) a method of defining a set of compounds that modulate the expression of a LNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds can be used for the generation compounds is used to identify nucleic acid sequences that are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAY52701 to AAX52704 represent sequences used in the exemplification of the present invention
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This nucleotide sequence comprises human CD40 antigen cDNA. It was isolated by a novel method for cloning cDNAs from mammalian expression libraries that is based on transient expression of an antigen in cutaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate, such as a culture dish. The method is useful for the isolation and molecular choning of any protein which can be expressed and transported to the cell surface membrane of a cutaryotic cell surface antigens such as CD1a, CD1, CD2, CD6, CD7, CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27, CD23, CD14, CD16, CD17, CD23, CD24, CD28, CD13, CD14, CD16, CD17, CD28, CD27, CD28, CD27, CD28, CD28
                     cDNA encoding human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expressing vectors for expression in eukaryotic cells or their fragments.
CAGGAGACACTGCACGGGTGTCAGCCTGTCACACAGGAGGATGGTAAAGAGAGTCGCATC
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Aruffo A;
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ilarity 62.7%; Pred. No. 3.9e-79;
Conservative 0; Mismatches 231;
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Simmons D, Aruf
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Allen J,
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89US-00379076.
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90US-00553759.
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Lauffer L,
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This invention describes novel pure proapoptotic dependence peptides
which comprise a sequence of an active dependence domain selected from
dependence polypeptides consisting of p75NTK, androgen receptor, DC.
thuringtin polypeptide, Machade-Joseph disease gene product, SCA1, SCA2,
SCA6 and atrophin-1 polypeptide. The proapoptotic peptides are capable of
inducing cell death and can be used to develop products to madiate or
inhibit apoptosis. The methods can be used for reducing the severity of a
proapoptotic dependence domain mediated pathological conditions e.g.
thurington's disease, Alzhelmer's disease, Kennedy's disease,
Coseph disease, stroke or head trauma. They can also be used for reducing
the severity of a pathological condition mediated by upregulated cell
proliferation or cell survival e.g. neoplastic, malignant, autoimmune or
fibrotic conditions. This sequence encodes the human CD40 polypeptide
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atrophin-1; cell death; apoptosis; Huntington's disease; head trauma; Alzheimer's disease; Kennedy's disease; spinocerebellar ataxia; stroke; dentatorubropallidoluysian atrophy; cell prollferation; cell survival; neophastic; malignant; autoimmune; fibrotic; CD40; ss.
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treating, e.g. Alzheimer's disease.
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48. .881
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The present sequence is that of cDNA encoding human cell surface antigen (CSA) CD40. The CDNA was isolated using a rapid immunoselection cloning method of the invention, designed to isolate CSA cDNAs. The method is based upon transient expression of a CSA in enkaryctic cells and physical selection of cells expressing the antigen by adhesion to (panning on) an antibody-oated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune adiated infections, diseases, and disorders in animals, including humans. These disorders include asthma, immune-complex disease, amyloidosis, parasitic diseases
                                                                                                                      Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated infections or disorders, e.g. asthma, immune-complex disease, parasitic
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Pred. No. 3.9e-79;
0; Mismatches 231;
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01-DEC-1992;
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    CTCTATATCAAAAGGTGGTCAAGAAACCAAAGGATAATGAGATGTTACCCCCTGCGGCT
                                                                        GICITITATCAAAAAGGTGGCCAAGAAGCAACCAATAAGGCCCCCCACCCCAAGCAGCAGCA
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AA247685 to AA247768 represent phosphorothicate antisense oligomuclectides targeted to human CD40, which can be used to inhibit the expression of human CD40. CD40 is involved in lymphocyte activation, tumour growth and/or angiogenesis. Inhibition of CD40 is used to treat or prevent immune-associated diseases (specifically guest vs. host disease, allograft rejection or autoimmune diseases); inflammation (specifically asthma, rheumatoid arthritis, allograft rejection, inflammatory bowel disease or psoriasis) or hyperproliferation (specifically cancer and tumours). The antisense oligomuclectides are also useful as diagnostic and research reagents. AA247769 represents the human CD40 nucleotide sequence. AA24770 to AA247769 represent human CD40 forward and reverse PCR primers, and a human CD40 Primers and a prose used in the exemplification of the present invention

1004 BP; 230 A; 297 C; 276 G; 201 T; 0 U; 0 Other;

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Itoh,M., Konno,H., OKazaki,Y., Muramateu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
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TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
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BUS16152 AGENCOURT
BY751423 BY751423
BY743050 BY743050
                                                                                                                                                                                   July 24, 2004, 23:50:12; Search time 2499 Seconds (without alignments) 9667.269 Million cell updates/sec
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                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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JOURNAL MEDLINE PUBMED

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/db_xref="c1:26354703"

/translation="MYSIPRICALMGCLLTAVHLGQCVTCSDKQYLHDGQCCDLCQPG
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CTCKBGQHCTSKDCGRACAQHTPCIPGEPGWNRATETTDTVCHPCPVGFFSNOSSLFEK
CYCKBGQHCTSKDCBACAQHTPCIPGIPGIPGKSRNRALEYIPVWGILITIFGVFIYIKKV
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                                                                                                                                                                                                                                                                                                                              86;
                                                                                                                                                                                                                                                                Score 679; DB 11; Length 2901;
Pred. No. 1.2e-196;
); Mismatches 0; Indels 86
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                                 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashino,H., Itoh,M., Sumi,N., Ishi,I.Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapilary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to Division of Experimental Animal Research in Riken contributed to Trust was were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust MRC building Addenbrookes Hospital Cambridge) whose Please visit our web site for further details.

URL:http://fantom.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium and the RIXEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation Of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2901)
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                                                                                                                                                                                                                                                                                                                                                                                 The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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AGENCOURT_10120358 NIH_MGC_134 Mus musculus cDNA clone
IMAGE:6512860 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: David Rowe
CDNA Library Preparation: Dr. M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of thtp://image.llnl.gov
http://image.llnl.gov
Flate: LiAMN4085 row: k column: 05
High quality sequence stop: 723.
High quality sequence stop: 723.
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Best Local Similarity 89.4%; Pred. No. 3.6e-194;
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Mus musculus (nouse mouse)

Mus musculus

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CE 1 (bases 1 to 692)

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Ravasi, T., Reed, J.C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

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	asstrance we gratefully acknowledge.  Please visit our web site (http://genome.gsc.riken.go.jp) for further details. Location/Qualifiers 1. 692 /organism="Mus musculus" /mol type="mRNA" /strain="NOD" /db xref="taxon:10090" /clone="F930034E13" /tissue_type="activated spleen" /clone_lib="RIKEN full-length enriched, activated spleen"	### Match   61.2%; Score 494.8; DB 13; Length 692;
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Fax: Brail: genome-resgec.riken.go.jp,

Machi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P.,

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Direct Submission

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Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in Riken

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and Microbiology/Parasitology/Sepuscience Center Science Laboratory

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Anallysis of the mouse transcriptome based on functional annotation of 60,770 full. length cDNAs
                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
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macrophage"
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strain="C57BL/6d"

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/tissue_type="bone marrow"
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (201) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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URL:http://genome-gsc.riken.go.jp,
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Takeda,Y., Waki,R., Watahiki,A., Murata,M., Nakamura,M.,
Direct Submission.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ilssues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGGTGTCTTTGCCTCGGCTGTGCGCGCTATGGGGGCTGCTTGTTGACAGCGGTCCATCTA
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/clone_lib="RIXEN full-length enriched, bone marrow
macrophage"
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llarity 94.7%; Pred. No. 4.1e-131;
Conservative 0; Mismatches 4; Indels 24;
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/clone="1830091M24"
                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
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Nume muscoulus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CE (bazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.;

Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.;

Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.;

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Batalov, S.; Beisel, K.W.; Blake, J.A.; Bradt, D.; Brusic, V.;

Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T.A.;

Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gaasterland, T.;

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Kawaji, H.; Kawasawa, Y.; Kedzierski, R.M.; King, B.L.; Konagaya, A.;

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Ravasi, T.; Reed, J. C.; Reed, D.J.; Reid, J.; Ringwald, M.;

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Wang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zhmmer, A.; Carninoi, P.;

Hayatsu, N.; Hiroane-Kishikawa-Boris, A.; Masmura, M.;

Sakazume, N.; Sato, K.; Shiraki, T.; Waterston, R.; Lander, E.S.;

Rogers, J.; Birney, E. and Hayashizaki, Y.; Analysis of lunctional annotation

of 60,770 full-length conas
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BY751441 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830034K15 5', mRNA sequence.
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                               152 TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCTCTTGAGAAGACCCCAATGCCAC
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Marmalia, Eutheria; Rodentia; Sciurognathi; Muridae; Buteleostomi; Nammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bazdi, Y.) Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Paldarelli, R., Hill, D. P., Bult, C., Chothia, C., Corbani, L. B., Cousins, S., Dalla, B. Fursic, V., Chothia, C., Corbani, L. B., Cousins, S., Dalla, B., Dragani, T. A., Fletcher, C.F., Forrest, A., Gough, J., Grafimond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehhard, B., Lyons, P. A., Maglott, D. R., Nanthioni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Bevan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Sultana, R., Takenaka, Y., Red, D. J., Rangisawa, M., Schenaka, Y., Taylor, M. S., Teasdale, R.D., Tomita, M., Verardo, R., Wanger, L., Wahlestedt, C., Setou, M., Sato, K., Shinata, K., Manger, L., Wahlestedt, C., Wang, Y., Matanabe, Y., Wanger, L., Wahlestedt, C., Setou, M., Sato, K., Shinata, K., Sasaki, K., Saraki, K., Kawai, J., Alzawa, K., Sthiata, K., Stakawa, T., Konno, H., Nakamura, M., Sato, K., Shiraki, T., Wangawa, M., Yasunishi, A., Sasaki, E., Sasaki, D., Shibata, K., Shinata, M., Billai, R., Wayazaki, M., Waterston, R., Lander, E., Shinata, M., Bander, E., Shinada, M., Bander, E., Shinada, M., Bander, C., Sasaki, K., Sasaki, C., Shibata, K., Shinata, M., Bander, E., Shinada, M., Bander, E., Shinada, M., Bander, C., Sasaki, K., Sasaki, M., Sado, M., Waterston, R., Sasaki, C., Sasaki, K., Sasaki, M., Shinata, M., Bander, M., Sado, M., Bander, M., B
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                                               -----ATCAAGGGCTTCGGGTTAAG 316
                                                                                                                 Rogers, J., Birney, E. and Hayashızaxı, r.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-81: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                      377 AGCAAGGATTGCGAGGCATGTGCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG 436
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BY744299 RIKEN full-length enriched, bone marrow macrophage Musmusculus cDNA clone 1830030F13 5', mRNA sequence.
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                                           AGACACTGTGAACCCA--
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format squencing pipeline with 384 multicapillary Sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length CDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose
                                                                                                                                                                                                                                                                                                        Email: genome-resegsc.riken.go.jp,

Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,

Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,

Furuda,S., Korno,H., Koya,S., Miyazaki,A., Murata,M., Kojama,Y.,

Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,

Nomura,K., Numazaki,R., Ohno,M., Obsato,N., Saito,R., Sakazume,N.,

Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., Tagami,M.,

Direct Submission
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/tissue_type="activated spleen"
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Please visit our web site (http://genome.gsc.riken.go.jp)
further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
                                                                     Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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DRIGIN

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Mammalia, Eutheria; Rodentia; Sciurognath; Muridae; Murinee; Mus. Rasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Oustons, S., Braito, D., Brasico, W., Enstelli, R., Hill, D. P., Bult, C., Golobori, T., Schrimi, L. M., Kanapin, A., Batsuda, H., Batalov, S., Beisel, K., W., Blake, J.A., Bradt, D., Brusico, W., Chothia, C., Corbani, L. B., Cousins, S., Dalla, B., Dragani, T. A., Gustincich, S., Hirokawa, N., Terzer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Karoin, I. W., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Namata, K., Okido, T., Partad, B. L., Maglott, D.R., Murata, K., Okido, T., Partad, G., Pescole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Sectou, M., Shinada, K., Sulming, L.G., Wanger, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Warasu, Y., Wang, Y., Warasu, M., Hirozane-Kishikawa, T., Yang, K., Yang, Sakatu, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Sasaki, D., Sabaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Land Hayashizaki, Y., Ragawa, I., Mayazaki, A., Sasaki, D., Sabaki, D., Shibata, K., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY745292 RIKEN full-length enriched, bone marrow macrophage Mus musculus cDNA clone 1830083N08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Arzawa,K., Akimura,T., Arzawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Namo,H., Numazaki,R., Ohno,M., Ohosto,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                     366 AGCAAGGATTGCGAGGCATGTGCTCAGCACGCCCTGTATCCCTGGCTTTGGAGTTATG 425
                                                                                                            GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGCCTTCTTCTCC 480
                                                                                                                                                                           426 gagangeccacheagaccacheanacearcherererecereceagregerrerere 485
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
481 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAG 529
                                                                                                                                                                                                                                                                                               486 AATCAGTCATCACTTTTCGAANAGTGTTATCCCTGGACAAGCTGTGAGG 534
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Mus musculus
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KEYWORDS
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BY745292
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                                                                                                                                                                                                                                                                                                                  Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new ganes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Rayloration Research Group in Riken Connel Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Tissues were project of Genome Rayloration Research contributed to prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Bukuda,S., Hashizume,M., Hayashida,K., Hirozane,T., Hori,P.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kwai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Matahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 AGCAAGGATTGCGAGGCATGTGCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG 420
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/clone_lib="RIKEN full-length enriched, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 463.6; DB 13; Length 649;
Pred. No. 8.3e-131;
0; Mismatches 5; Indels 24;
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/clone="1830030F13"
/tissue_type="bone marrow"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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/strain="C57BL/6J"
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601776584F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4018221 5',
mRNA sequence.
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Mus musculus
Mus musculus
Mus musculus
Muscardes, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Musmmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
Mut-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="spontaneous tumor, metastatic to mammary. Stem cell origin."
/lab host="Dright"
/clone lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/ibrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCTCTTGAGAAGACCCAATGCCAC 180
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM9268 row: g column: 22

High quality: sequence stop: 668.

Location/Qualifiers
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            484 AATCAGTCATCACTTTTTGAAAAGTGTTATCCCTGGACAAGCTGTGAGG
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4018221"
                                                                                                                                                                                                                                                         BF166137.1 GI:11046489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.6%;
Matches 495; Conservative
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Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

noryclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Construction of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by David A. Hume (Depts. of Biochemistry

and Microbiology/Parasicology/ Institute for Molecular Bioscience

assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details
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/clone="1830083N08"
/tissue type="bone marrow"
/cell_type="macrophage"
/clone lib="RIKEN full-length enriched, bone marrow
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/strain="C57BL/6J"
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ENCARTOCAS, METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(E. (basaki, Y.; Puruno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.; Saito, R.; Suzuki, H.; Yamanaka, I.; Kayosawa, H.; Yagai, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Cayobori, T.; Baldarelli, R.; Hill, D.P.; Bult, C.; Gojobori, T.; Baldarelli, R.; Hall, D.P.; Bult, C.; Corbani, L.E.; Cousins, S.; Dalla, B.; Dragani, T.A.; Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gaasterland, T.; Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gaasterland, T.; Fletcher, C.F.; Forrest, A.; Frazer, K.S.; Gaasterland, T.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Redzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Redzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Redzierski, R.M.; King, B.L.; Konagaya, A.; Kawaji, H.; Kawasawa, Y.; Reed, J.C.; Redci, J.; Pertea, G.; Pescle, G.; Pertea, G.; Pescle, G.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                      363
                                                                                                           420
                                                                                                                                                                            423
                                                                                                                                                                                                                                                     480
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URL.http://genome.gsc.riken.go.jp/
Adachi,J., Azawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
                                      AGCAAGGATTGCGAGGCATGTGCTCAGCACGCCCTGTATCCCTGGCTTTGGAGTTATG
                                                                                                                                                 421 GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTTCTCC
484 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGCTGTGAGG 532
                                                                                                                                                                                                                                                                                                                                                                                                   481 AATCAGTCATCATTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAG
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BY745260.1 GI:27172371
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TITLE

COMMENT

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Direct submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RIGA) system--384-format sequencing pippeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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/clone lib="RIKEN full-length enriched, bone marrow
macrophage"
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/clone="1830083B08"
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/strain="C57BL/6J"
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                                                                                                                                                 CB547441
AMGNNUC:NRDG1-00106-F8-A nrdg1 (10855) Rattus norvegicus CDNA clone nrdg1-00106-f8 5', mRNA sequence.
81 GGACAGTGTGTTACGTGCAGTGACAAACAGTACCTCCAAGGTGGCGGGTGCGATTTG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCAGTGTGTTACGTGCAGTGACAAACAGTACCTCCACGATGGCCAGTGCTGTTTG 120
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                                                                                                                                                                                                                                             Rattus norvegicus
Rattus norvegicus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteléostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10|16"
/db_orse="nordel-00106-f8"
/tissue_type="Dorsal Root Ganglia"
/clone=lib="nordel (10855)"
/nore="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; ratters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGTGTCTTTGCCTCGGCTGTGCGCCTATGGGGCTGCTTGTTGACAGCGGTCCATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881

Plate: 00106 row: f column: 8.
Location/Qualifiers
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                                              481 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAG 529
                                                                                534
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47.0%; Score 380.6; DB 14; Length 603;
Best Local Similarity 83.7%; Pred. No. 2.6e-105;
Matches 453; Conservative 0; Mismatches 64; Indels 24;
                                                               487 -ATCAGTCATCACTTTTCGAAAAGTGTATCCCTGGACAAGCTGTGGGG
                                                                                                                                                                                                                                                                                                         Rattus.
1 (bases 1 to 603)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
                                                                                                                                                                                                                  CB547441.1 GI:29431382
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Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Tissues were provided by Dr. John Todd (Dept. of Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="maxAx"
/mol_type="maxAx"
/strain="NOD"
/db_xref="taxon:10090"
/db_xref="F830006N20"
/i.Ssue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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CLORE 1720015002 5', MRNA sequence.

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BY 1720 RICKEN FILL-Length enriched, TIB-55 BBS Nus musculus CDNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-45-503-9222
Fax: 81-45-503-9216
Fax: 81-45-503-9226
Fax: 81-45-503-9226
Fax: 81-45-503-922
Fax: 81-45-503-923
Fax: 81-45-503-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(62C), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/mol_type="mRNA"
/strain="NOD"
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/clone="F830006D03"
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hassgawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Eatalov, S., Beisel, K. W., Blake, J. A., Brast, D., Brusic, V., Chothia, C., Corbani, L. B., Cousins, S., Dalla, E., Dragani, T. A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
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                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/clone="730019D02"
/cell_line="TIE-55 BB88"
/clone_lib="RIKEN full-length enriched, TIB-55 BB88"
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details
Location/Qualifiers
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a norredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Center for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistence we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details. /tissue\_type="activated spleen" /clone\_lib="RIKEN full-length enriched, activated spleen" Length 429; Score 355; DB 13; Pred. No. 1.6e-97;

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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozanie,T., Indetani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence dustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Division of Experimental Animal Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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1-7-22 Suebhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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/clone="K39004F09"
/clone_lib="RIKEN full-length enriched, visual cortex"
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/organism="Mus musculus"
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/strain="C57BL/6J"
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RS (Mazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Godobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schrimi,L.M., Kanapin,A., Matsuda,H., Patecher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Garibold,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gastincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanaja,H., Kawasawa,T., Rodzik,A., Gough,J., Grimmond,S., Kavaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Maglott,D.R., Waltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Nackon,I.J., McKenzie,L., Miki,H., Nagashima,T., Nackod,J.C., Perce,G., Pesole,G., Perchantan,S., Sandelin,A., Schneider,C., Reed,D.J., Ring,S., Margis,L., Manger,L., Wallais,R., Pontius,J.U., Qi,D., Ramachandran,S., Sandelin,A., Schneider,C., Wallais,G., Wang,Y., Watanabe,Y., Verardo,R., Wagger,L., Wallested,C., Wang,Y., Watanabe,Y., Vang,Y., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Wallais,C., Wilming,L.G., Whishaw-Boris,A., Yang,Y., Maramae,K., Shibaka,K., Sakazume,N., Hirozane-Kishkawa,T., Kawai,J., Alazawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Inbii,Y., Arakawa,T., Fukuda,S., Hara,A., Sakai,K., Sasaki,D., Shibata,K., Arakawa,T., Shibata,K., Sakazume,N., Sakazume,N., Sakazume,N., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,K., Sakai,C., Shibata,K., Sakai,K., Sakai
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GenCore version 5.1.6
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                                                                                   Query Match 100.0%; Score 809; DB 6; Length 809; Best Local Similarity 100.0%; Pred. No. 2.9e-244; Matches 809; Conservative 0; Mismatches 0; Indels
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MAU401387 869 bp mRNA linear ROD 01-JUN-2001 Mus musculus mRNA for CD40 type II isoform (CD40 gene).

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/db_xref="G04:227512"
/db_xref="SWISS-PROT:P27512"
/db_xref="SWISS-PROT:P275
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                                                                                                                                                                                              Craniata, Vertebrata, Euteleostomi;
Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AGACACTGTGAACCCA------ATCAAGGGCTTCGGGTTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (19-JJL-2000) Tone M., Sir William Dunn School of
Pathology, University of Oxford, South Parks Road, Oxford, OXI
UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 GGGCAGTGTGTTACGTGCAGTGACAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG
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                                                                                                                                                                                                                                                                                                Tone, M., Tone, Y., Fairchild, P.J., Wykes, M. and Waldmann, H. Regulation of CD40 function by its isoforms generated through alternative splicing
Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)
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AJ401387
AJ401387.1 GI:13016729
alternative splicing; CD40 gene; CD40 type
Mus musculus (house mouse)
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/note="alternative transcript"
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/mol_type="mRNA"
/db_xref="taxon:10090"
1. 869
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Matches 785;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

E. 1 (Bases 1 to 870)

RS 1 to 870)

Indrovement in tolerance to xenografts

AL Patent: JP 200523115-A 5 02-0CT-2002;

MLIABERATORIES PLC

OS Mus sp. (mouse)

PN 17-DEC-1999 JP 2000589212

PR 17-DEC-1999 GB 9827921.9; PR 17-DEC-1999 GB 9825015.1 PI

ROBERT IAN LECHLER, NICHOLA JANE ROGERS, ANTHONY DORLING PC

CLIANIS/O9, AGIRSSY/O6, AGIRSSY/O6, CO7NIG6/28, CI2P21/O8, CI2NIS/O0 CC

Improvement in tolerance to xenografts

FR Key Location/Qualifiers

FT Source Location/Qualifiers

FT Fource Location/Qualifiers
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AGACACTGTGAACCCAGTGCGTGGGGTGCCTGGGAAGGGATCAAGGGCTTCGGGTTAAG 300
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                                                                                                                                                                                                             GAGATGGCCACTGAGACCACTGATACCGTCTCTCTCTCCCCCCAGTCGCCTTCTTCTCC
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                                                                     AGCAAGGATTGCGAGGCATGTGCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG
                                                                                                                                                                                                                                                                                                                         457 AATCAGTCATCACTTTTCGAAAAGTGTTAATCCCTGGACAAGGTTTAAAGTCCCGGATGCG
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                                                                                                                                                                                                                                                                                        AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCG
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/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"
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                                  241 ÁGÁCACTGTGAACCCA----
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JP 2002532115-A/5.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                ACGGCAAGATCCCCCAGGAGATGGAAGATTATCCCGGTCATAACACGCTGCTCCAGTGCA
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                                  403 GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTCTCC
                                                                                  AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCG
                                                                                                                                                                                                                              CTATATCAAAAAGGTGGTCAAGAAACCAAAGGATAATGAGATGTTACCCCCTGCGGCTCG
                                                                                                                                                                                                                                                    GGAGACACTGCACGGGTGTCAGCCTGTCACACAGGAGGATGGTAAAGAGGAGTCGCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                           CCATGTGACTCAGGCGAATTCTCAGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCAC
           GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCTGCCCAGTCGGCTTCTTCTCC
                                                                                                                   463 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAAGTCCCGGATGCG
                                                                                                                                                       AGCCCTGCTGGTCATTCCTGTGATGGGCATCCTCATCACCATTTTCGGGGGTGTTTCT
                                                                                                                                                                                                                                                                                                                                        643 ACGCCAGATCCCCAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTGCA
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Pred. No. 4.7e-223;
0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTGCAGGAGGCGCAGGTGACAGACAGCA 791
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Sequence 4 from Patent WO0105967.
AX077880
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Best Local Similarity 97.0%;
Matches 776; Conservative
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Homo sapiens
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AX077880
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Immunosuppression
Patent: WO 0037102-A 11 29-JUN-2000;
ROGERS NICHOLA JANE (GB); DORLING ANTHONY
LECHLER ROBERT IAN (GB)
Location/Qualifiers
1. 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCAGTCATCACTTTCGAAAAGTGTTATCCCTGGACAA-
                                                                                                                                                                     Score 679; DB 6; L
Pred. No. 4.1e-203;
0; Mismatches 0;
                                                     Rogers, N.J., Dorling, A. and Lechler, R.I.
                                                                                                                      /organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
      Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Best Local Similarity 90.1%;
Matches 785; Conservative (
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                                                                    GAGATGGCCACTGAGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCCTTCTTCTCC
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                                                                                             GGGCAGTGTTACGTGCAGTGACAAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG
                                                                                                        GGGCAGTGTGTTACGTGCAGTGACAAAAAGTACCTCCACGATGGCCAGTGCTGTGATTTG
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                                                                                                                                                                         CCATGTGACTCAGGCGAATTCTCAGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCAC
                                                                                                                                                                                                                                AGACACTGTGAACCCA-------AGACACGGTTCGGGTTAAG
                                                                                                                                                                                                                                                                                                                               GAGATGGCCACTGACCACTGATACCGTCTGTCATCCCTGCCCAGTCGGCTTCTTCTCC
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                                       Gaps
                                       86;
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                   Length 870;
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                                    0; Indels
                 Score 679; DB 6; 1
Pred. No. 4.1e-203;
0; Mismatches 0;
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Sequence 11 from Patent W00037102.
AX027014
AX027014.1 GI:10188044
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                   83.9%;
90.1%;
                    Query Match
Best Local Similarity 90.1
Matches 785; Conservative
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Nus musculus (house mouse)

Nus musculus (house mouse)

Nus musculus

ENkarycta; Metazoa; Chordata; Sciurognath; Muridae; Murinae; Musculus

Enkarycta; Metazoa; Chordata; Sciurognath; Muridae; Murinae; Musculus

Straubsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Buromstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Morkernan, K.D., Mullahy, S.J., Guaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Butterfield, Y.S., Krzywinski, M., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M., Salska, U., Sanilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

No. 22388257
                                                                                                           ROD 07-OCT-2003
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24850128.
                                                                                                        BC029254 1281 bp mRNA linear ROD 07-OCT-2003
Mus musculus tumor necrosis factor receptor superfamily, member 5, mRNA (cDNA clone MGC:36032 IMAGE:4018221), complete cds
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/clone="MGC:36032 IMAGE:4018221"
/tissue_type="Mammary tumor metastatized to lung. Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-WGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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/mol_type="mRNA"
/strain="CZECH II"
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CTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEK
CTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEK
VEYPTSCEDKYLEVLQKGTSQTNVICGLKSRNRALLVIPVVMGILITIFGVPIYIKKV
VKKPKNDSIJALPPAARRQDPQEMEDYFGHNTAAPVQETLHGCQPVTQEDGKESRISVQE
RQVTDSIJALRPLV"
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/gene="CD40"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCAGCCAGGAAGCCGACTGACAAGCCACTGCACAGCCACTTGTTGAAGAAGACCCAATGCCAC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATGTGACTCAGGCGAATTCTCAGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCAC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATGTGACTCAGGCGAATTCTCAGCCCAGTGGAACAGGGAGATTCGCTGTCACCAGCAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AGACACTGTGAACCCAGTGCGTGGGCTGCCTGGGAAGGGATCAAGGGCTTCGGGTTAAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 caddadacactdcacdgcardrcaccacacacacacacardaraaaaaaacacarc 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGIGICTTTGCCTCGGCTGTGCGCGCTATGGGGCTGCTTGTTGACAGCGGTCCATCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 AGCAAGGATTGCGAGGCATGTGCTCAGCACACGCCCTGTATCCCTGGCTTTGGAGTTATG
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                     Score 679; DB 10; Length 1579;
Pred. No. 4.4e-203;
0; Mismatches 0; Indels 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGTGCAGGAGCGGCAGGTGACAGACAGCA 855
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                                                                                                                                                                                                                                                                        83.9%;
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.13
Matches 785, Conservative
                                                                                                                 polyA_signal
                                                                                                                                                                     polyA_site
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CYPWTSCEDRNLEVLQKGTSQTNV1CGLKSRNRALLVIPVVMGILITIFGVFFLXISGQ
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909
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Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                        CGACGGCAAGATCCCCCAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTG
547 GAGGTCCTACAGAAAGGAACGAGTCAGACTAATGTCATCTGTGGTTTAAAGTCCCGGATG
                                                                                                                                       CTCTATATCAAAAAGGTGGTCAAGAAACCAAAGGATAATGAGATCCTACCCCTGCGGCT
                                                                                                                                                                                                                                                                                   CTCTATATCAAAAAGGTGGTCAAGAAACCAAAGGATAATGAGATGTTACCCCCTGCGGCT
                                                                                                                                                                                   CGACGGCAAGATCCCCCAGGAGATGGAAGATTATCCCGGTCATAACACCGCTGCTCCAGTG
                                                                                                                                                                                                                                                            CAGGAGACACTGCACGGGTGTCAGCCTGTCACACGAGGATGGTAAAGAGAGTCGCATC
                                   CGAGCCCTGCTGGTCATTCCTGTCGTGATGGGCATCCTCATCACCATTTTCGGGGGTGTTT
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Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)
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South Parks Road, Oxford, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternative splicing; CD40 gene; CD40 type IV isoform. Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Bu
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMU401389 926 bp mRNA linear RC
Mus musculus mRNA for CD40 type IV isoform (CD40 gene)
AJ401389
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Pred. No. 8.9e-197;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CD40"
/note="alternative transcript"
                                                                                                                                                                                                                                                                                                                                  TCAGTGCAGGAGCGGCAGGTGACAGACAGCA 809
                                                                                                                                                                                                                                                                                                                                                                        877
                                                                                                                                                                                                                                                                                                                                                            TCAGTGCAGGAGCGGCAGGTGACAGACAGCA
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Submitted (19-JUL-2000) Tone M.,
Pathology, University of Oxford,
UNITED KINGDOM
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1. .926
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89.6%;
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Best Local Similarity 89.6
Matches 780; Conservative
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DEFINITION
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AUTHORS
TITLE
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TITLE
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MMU401389
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                                                                                                                               IMD3, TRAP, HIGM1,
                                                                                                                                                                                                                                                                                                                                                                                                                             343. .459
/note="TNFR, Region: Tumor necrosis factor receptor /
nerve growth factor receptor repeats in growth
factor receptors that are involved in growth factor
binding. TNF/TNFR"
/db_xref="CDD:smart00208"
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arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." (clone_lib="NCI_GAP_Lu29" (lab_host="nBl10B")
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                                                                                                                              note="synonyms: IGM, p50, Bp50,
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Pred. No. 4.9e-199;
0; Mismatches 8;
                                                                        'note="Vector: pCMV-SPORT6"
                                                                                                                                                                 /db_xref="LocusID:21939"
/db_xref="MGI:88336"
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                                                                                                              'gene="Tnfrsf5"
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אמה אוא museulus mRNA for CD40 type V isoform (CD40 ge. AJ401390

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 10 MMU401390

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/ codon start="">
// product="cD40 type V isoform"
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Tone,M., Tone,Y., Fairchild,P.J., Wykes,M. and Waldmann,H. Regulation of CD40 function by its isoforms generated through alternative splicing Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001) 21117110
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                                                                                                                                                                                                                                                                                                                 Sir William Dunn School of
South Parks Road, Oxford,
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/gene="CD40"
/note="alternative transcript"
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/organism="Mus musculus"
/or_type="mRNA"
/db_xref="taxon:10090"
1. .844
/gene="CD40"
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Direct Submission
Submitted (19-JUL-2000) Tone M.,
Pathology, University of Oxford,
UNITED KINGDOM
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alternative splicing; CD40 gene; CD40 type V isoform.
Muss musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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South Parks Road, Oxford, OX1 3RE,
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Proc. Natl. Acad. Sci. U.S.A. 98 (4), 1751-1756 (2001)
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Mus musculus (house mouse)
Mus musculus
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Mus musculus mRNA for CD40 type III isoform (CD40 gene)
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/organism="Mus musculus"
/mol_type="mRNA"
/db_tref="taxon:10090"
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Submitted (19-JUL-2000) Tone M.,
Pathology, University of Oxford,
UNITED KINGDOM
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                                                                                  Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                             Query Match 67.6%; Score 547; DB 6; Length 788; Best Local Similarity 95.3%; Pred. No. 2.5e-161; Matches 584; Conservative 0; Mismatches 5; Indels
  linear
    DNA
                                                                                                                                      Savitzky, K., Khosravi, R. and Blazar, M. Splice variants of cd40-receptor Patent: WO 0105967-A 5 25-JAN-2001; Compugen Ltd. (IL)
                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
 AX077881 788 bp Sequence 5 from Patent WO0105967.
                                          AX077881.1 GI:13157728
                                                                       sapiens (human)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 GGGCAGTGTTACCTGCAGTGACAAACAGTACCTCCACGATGGCCAGTGCTGTGATTTG
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                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                            Length 934;
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Rattus norvegicus CD40 protein mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                         Score 429.2; DB 6;
Pred. No. 4.9e-124;
0; Mismatches 43;
                                                               Savitzky, K., Khosravi, R. and Blazar, M. Splice variants of cd40-receptor Patent: WO 0105967-A 3 25-JAN-2001; Compugen Ltd. (IL)
                                                                                                                                                                             1. .934
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AF241231
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PAT 14-JUL-2003
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Novel genetic markers for leukemias Novel genetic markers for leukemias Patent: WO 03039443-A 2460 15-Wax-2003;
Deutsches Krebsforschungszentrum (DB);
Ludwig-Maximilan-Universitaet Muenchen (DB); Haferlach, Torsten, PD Dr. Dr. (DB); Schoch, Claudia (DE);
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                AGCAAGGATTGCGAGGCATGTGCTCAGCACGCCCTGTATCCCTGGCTTTGGAGTTATG
                                                                                           377 AGCAAGGAGTGCGAGACGTGCGCTCAGCACAGGCCCTGTGGCCCTGGCCTTTGGAGTCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AX780303 1114 bp DNA
Sequence 2460 from Patent W003039443.
AX780303.1 GI:32697297
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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NRLVSHCTALEKTQCQPCDSGBFSAHWNREIRCHQHRHCELNQGLQVKKEGTAVSDTV
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                         Krzesz,R., Wagner,A.H., Cattaruzza,M. and Hecker,M.
Cytokine-inducible CD40 gene expression in vascular smooth muscle
cells is mediated by nuclear factor kappaB and signal transducer
and activation of transcription-1
FEBS Lett. 453 (1-2), 191-196 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-MAR-2000) Dept. of Cardiovascular Physiology, of Goettingen, Humboldtallee 23, Goettingen 37073, Germany (a Chases I to 547)

Direct Submission. M.

Direct Submission. of Cardiovascular Physiology, Submitted (21-MAR-2011) Dept. of Cardiovascular Physiology, of Goettingen, Humboldtallee 23, Goettingen 37073, Germany Sequence update by submitter

On Mar 21, 2001 this sequence version replaced gi:7248905.
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/protein_id="AAF43717.2"
/db_xref="G1:13400108"
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Rattus norvegicus
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/strain="Wistar"
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                                                                                   481 AATCAGTCATCACTTTTCGAAAAGTGTTATCCCTGGACAAGGTTTAAAGTCCCGGATGCG 540
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Search completed: July 25, 2004, 02:42:48 Job time : 3302 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

July 21, 2004, 10:03:39 ; Search time 16 Seconds (without alignments) 961.915 Million cell updates/sec Run on:

US-10-031-607-7 913 1 MVRLPLQCVLWGCLLTAVHP......WLCNRQAQTRLMLSVVPRIG 160 Title: Perfect score:

Sequence:

Scoring table: BLOSUM62 Gapox 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CTIMMADIES

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ະ ເຄີ	Score		H	DB		Description
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۲۷	483	52.9	0	~	A46476	B cell-associated
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80	173	ω,	7	~	B38634	tumor necrosis fac
σ	7	œ.	4	7	D72175	G2R protein - vari
10	7	ω.	4	7	D36858	gene G4R protein -
11	167.5		9	н	A46517	CD27 antigen precu
12	67.	œ	4	~	T28623	hypothetical prote
13	165		m	N	A40036	apoptosis-mediatin
14	S	è.	-	(7	137383	FAS soluble protei
15	S	ė.	S	-	A49053	antigen
16	4	Š.	~	7	S12783	ρι
17	4		-	N	I48700	ox40 prc
18	•	14.8	277	~	137552	homolog
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21	N	14.1	N	-	GQVZML	놑
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23	125.5		S	-	GOHUTI	tumor necrosis fac
24	$^{\circ}$	13.3	S	α	JC7705	ath recepto
25	М		$^{\circ}$	7	B43692	T2 protein - rabbi
56	•	12.7	$^{\circ}$	Н	GOHON	
27	$\vdash$		1069	~	T42681	hypothetical prote
28	ď.	12.0	461	7	JC4302	crosi
29	99.	12.0	7	~	4201	cysteine rich prot

121 LHRSCSPGFGVKQIAVRPKTWLC 143 

CD 8

nerve growth facto CDw40 antigen Hu54	neurogenic protein	gene Delta protein	neurogenic repetit	laminin beta-1 cha	odz protein - frui	tenascin-like prot	gene PACE4 protein	serine proteinase	mucin, submaxillar	protein C34G6.2 [i	Nel-homolog protei	PACE4A - mouse (fr	Delta-4 protein -	Delta-4 protein -
A26431 B60771	A31246	S19087	800670	MMFFB1	A54148	S47008	I53282	S34583	T03099	F87789	T10756	I52527	JC7569	JC7570
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108.5	107	107	107	107	106	106	105	103.5	103.5	103	103	101	100.5	100

## ALIGNMENTS

RESULT 1 A60711 B-cell activation protein CD40 precursor - human N;Alternate names: B-cell surface antigen Bp50 C;Species: Homo sapiens (man) C;Acces: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000 C;Accession: S04460; A60771 R;Stamenkovic, I; Clark, B.A.; Seed, B.//	EMBO J. 8, 1403-1410, 1989  A,Trile: A B-lymphocyte activation molecule related to the nerve growth factor receptor & A,Reference number: \$04460; MUID:89386608; PMID:2475341  A,Reference number: \$04460  A;Rocession: \$04460  A;Rosidues: 1-277 <sta>  A,Residues: 1-277 <sta>  A,Cross-references: BEBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851  R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.</sta></sta>	J. Immunol. 142, 562-567, 1989 J. Immunol. 142, 562-567, 1989 J.Title: Blochemical characteristics and partial amino acid sequence of the receptor-like A, Fitle: Blochemical characteristics and partial amino acid sequence of the receptor-like A, Reference number: A60771, MUID:89093941; PMID:2463309 A, Accession: A60771 A, Molecule type: protein A, Residues: 21-50 cBRA> A, Experimental source: Burkitt lymphoma cell line Raji C, Genetics: C, Genetics: A, Genetics:	A,Cross-references: GDB:215268; OMIM:109535 A,Map position: 20012-200413.2 A,Map position: 20012-200413.2 C,Superfamily: CD27 antigen; NGF receptor repeat homology C,Superfamily: CD27 antigen; Phosphoprotein, Surface antigen; transmembrane predicted <sig- #status="" <nat="" activation="" b-cell="" cd40="" experimental="" f;21-277="" product:="" protein=""> F;21-277/Product: B-cell activation protein CD40 #status experimental <nat> F;21-277/Domain: extracellular #status predicted <nt> F;216-277/Domain: intracellular #status predicted <cyt> F;216-277/Domain: intracellular #status predicted <cyt> F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted</cyt></cyt></nt></nat></sig->	Query Match Best Local Similarity 95.1%; Pred. No. S.8e-57; Matches 136; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  Qy	Oy 61 PCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCV 120
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A;Residues: 23.461 CEEN.
A;Cross-references: GB:S63369; NID:g235648; PIDN:AAB19924.1; PID:g235649
A;Cross-references: GB:S63369; NID:g235648; PIDN:AAB19924.1; PID:g235649
A;Cross-references: GB:S63369; NID:g235648; PIDN:63368, NCBID:63351)
B;Cross-references: R.A.; Song, K.; Chasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat.
A;Reference number: A36007; WUID:90349572; PMID:2166946
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C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
C;Reywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/pomain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NGI>
F;78-119/Domain: NGF recepto
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Mydlecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 116-140, 'P' 142-195,'R', 197-362, 'T', 364-461 <HEL>
A, Cross-references: GB:M35857; NID:g3339751; PIDN:AAA63262.1; PID:g339752
R, Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
Biol. Chem. 265, 20131-20138, 1990
A, Ritle: Purification and partial amino acid sequence analysis of two distinct tumor necrement management of the contract of the contract
                                                                                                                  A,Cross-references: GB:M385994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758 R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Cytokine, Z. 231-237, 1990 A;A;Aitle: Two human TNF receptors have similar extracellular, but distinct intracellular, A;Reference number: A48416; MUID:91370690; PMID:1966549
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A;Molecule type: protein
A;Molecule type: protein
A;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence 1
A;Reference number: A35010; WUID:90110215; PMID:2153136
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A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
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A;Motecule type: protein
A;Motecule type: protein
A;Meesidues: 27-31 < ENG>
E;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of A;Reference number: 138094; MUID:95121934; PMID:7821811
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F1-12/Domain: signal sequence #status predicted <516>
F1-16/Domain: signal sequence receptor zeceptor 2 #status experimental F140-76/Domain: NGF receptor repeat homology <NG2>
F180-119/Domain: NGF receptor repeat homology <NG3>
F120-162/Domain: NGF receptor repeat homology <NG3>
F164-201/Domain: NGF receptor repeat homology <NG3>
F164-201/Domain: NGF receptor repeat homology <NG4>
F164-201/Domain: NGF receptor repeat homology <NG4>
F164-201/Domain: NGF receptor repeat homology <NG4>
F166-219/Domain: NGF receptor repeat homology <NG4>
F166-219/Domain: intracellular #status predicted <TMN>
F1711,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Molecule type: mRNA
A,Residues: 1-195,'R',197-461 <KOH>
A,Cross-references: GB:MS5994; GB:M
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A; Molecule type: mRNA; protein
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A;Introns: 26/3
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Best Local Simi
Matches 51;
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N.Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: 435366; A36475; A48416; A36007; A22666; B35010; I38094
R.Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K Science 248, 1019-1023, 1990
A.Title: A receptor for tumor necrosis factor defines an unusual family of cellular and A, Receptor on the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                         R;Torres, R.M.; Clark, E.A.
2. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Coss. 1-461 < SMIA.
A;Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
B;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur A;Reference number: A36475; MUID:91045991; PMID:2172983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0.
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, B.A.; Howard, M.; Cockayne, Immunol. 149, 1921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
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A/Status: preliminary; not compared with conceptual translation
A/Status: preliminary; not caid
A/Rolecule type: nucleic acid
A/Rosidues: 1-287,'LV, <ARI->
A/CRSS-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:W94126;
A/Experimental source: BALB/c, liver
A/NOTE: sequence extracted from NCBI backbone (NCBIP:120357)
C/Comment: For an alternative splice form, see PIR:A46515.
C/Comment: For an alternative splice form, see PIR:A46516.
C/Superfamily: CD27 antigen; NGF receptor repeat homology
C/Reywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>
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                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
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                                                                                                                                       cell-associated surface molecule CD40, long splice form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:M83312; NID:g1553058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LHRSCSPGFGVKQIAVRPKTWLCN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 OHTPCIPGFGVMEMATETTDTVCH 144
                                                                                                                                                                                                                                                                                                                                                       C; Accession: A46476; A46515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule_type: mRNA
A;Residues: 1-305 <TOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A46515
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9 61 77 4 LPLQCVLWGCLLTAVHPEPPTACREKQYLINS - - QCCSLCQPGQKLVSDCTEFTETECLP 23 LPAGVA----FTPYAPEPGSTCRLREYYDQTAQMCCSKCSPGGHAKVFCTKTSDTVCDS Gaps 27;

5;

Gaps

11;

86

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apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1933 #sequence_revision 18-Nov-1994 #text_change 07-Jul-2003
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, A;Title: The CDNA structure, expression, and chromosomal assignment of the mouse Fas anti A;Reference number: A46484; MUID:92148151; PMID:1371136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:MB3649; NID:g193225; PIDN:AAB37593.1; PID:g193226
A;Experimental source: BAM3 macrophage cell line
Nocional sequence extracted from NGB locathone (NCBIN:81544, NCBIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of an early transposable element
A;Reference number: A47254; MUID:93189576; PMID:7680478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A;Experimental source: WRL lpr/lpr
A;Experimental source: WRL pr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863, C;Superfamily: tumor neorosis factor receptor type 1; NGF receptor repeat homology C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 HCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIA 135
                                                                                                                                                                                                                                                                                                                                                           79 QHKYCDPNIGLRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQI---A 135
                                                                                                                                                                                                                                                                                                                                                                                        21 EPPTACREKQYLINSQCCSLCQPGQKLVSDC-TEFTETECLPCGE-SEFLDTWNRETHCH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 VHPEPPTACREKQYLINSOCCSLCOPGOXLVSDCTEFTET-ECLPCGE-SEFLDTWNRET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 VH-EIDKNCSEGLYQGGPFCCQPCQPGKKKVEDCKNNGGTPTCAPCTEGKEYMDKNHYAD
                                                                                                                                                                                                                                                                               39 ETDNNCSEGLYQVGFFCCQPCQPGBRKVKDCTTSGGAPTCHPCTEGEBEYTDRKHYSDKCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                          Indels
F;22-324/Product: Fas antigen #status predicted <MAT> F;44-9f/Domain: NGF receptor repeat homology <NGF> F;81-124/Domain: NGF receptor repeat homology <NG4> F;81-124/Domain: GFF receptor repeat homology <NG4> F;171-188/Domain: transmembrane #status predicted <TWM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%; Score 180; DB 2;
llarity 33.6%; Pred. No. 1.2e-07;
Conservative 15; Mismatches 68
                                                                                                                                         Score 188.5; DB 2
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;44-79/Domain: NGF receptor repeat homology <NGF>F;81-124/Domain: NGF receptor repeat homology <NG4>
                                                                                                                    20.6%; Scor. 30.6%; Pred. No. 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 VRPKTWL----CNRQA-QTRLMLSVV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 VRPKTWLCNRQAQT -- RLMLSVVP 157
                                                                                                                                                                                                44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <ADA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                         Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-327 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A46484
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A,Molecule type: mRNA
A,Molecule type: Try <KI2>
A,Residues: 1-62, YRT' <KI2>
A,Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAR05109.1; PID:d1005651; PID:g468489
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fas antigen precursor - rat (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: Rattus norvegicus (Norway rat) (Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Jul-2003 (Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Jul-2003 (Species: Diophen, Diophen, Es. Commun. 199, 66-674, 1994 A; Kimura, K.; Wakatsuki, T.; Yamamoto, M. A; Reference number: Gommun. 199, 66-674, 1994 A; A; Action of Fas antigen in the rat live A; Reference number: JC2395; MUD:94128114; PMID:7507668 A; Accession: JC2395 A; MUD:94128114; PMID:7507668 A; Residues: 1-324 KIM> A; Residues: 1-324 KIM> A; Residues: DBBJ:D26112; NID:9468486; PIDN:BAR05108.1; PID:d1005650; PID:9468487 A; Accession: PC2246.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 FTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 INDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQPGMFCAA 134
                                                                   CGESEFLDTWNRETHCHQHKYCDPNLGLRVQ-----QKGTSETDTICTCEEGWHCT--- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PLQCVLWGCLLTAVHPE--PPTA----CR--EKQYLINSQ--CCSLCQPGQKLVSDCTE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLVLGLFG-LLAASOPOAVPPYASENOTCRDOEKEYYEPOHRICCSRCPPGTYVSAKCSR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.9%; Score 200; DB 2; Length 435 36.5%; Pred. No. 3.6e-09; tive 15; Mismatches 58; Indels
                                                                                                                                                                                                   131 OEGCRICAPLRKCRPGFGV----ARPGT 154
                                                                                                                                              113 SEACESCVLHRSCSPGFGVKQIAVRPKT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EA--CESCVLHRSCSPG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALECTHCELLSDCPPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Conservative
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Best Local Similarity
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9

Gaps

14;

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule to the EMBL Data Library, April 1995
A;Dolecule to the EMBL Data Library, April 1995
A;Description: Nuclectide sequence analysis of the region of Variola virus Xhol F O H P C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rishchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopare submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                  51 CTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGL-RVQQKG-TSETDTICTCEEG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 EFLDTWNRETHCHQ-HKYCDPNLGLRVQQKGTSET-DTICTCEEGWHCT---SEACESCV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFTSRNNHLPACLSCNGRCNSN---QVETRSCNTTHNRICECSPGYYCLLKGSSGCKACV 128
                                                                                                                                                                                                   67
                                                                                                                                 2 VRLPLQCVLWG------CLLTAVHPEPPTACREKQYLIN---SQCCSLCQPGQKLVSD 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LQCVLWGCLLTAVHPEPPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGES 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LSCIIINGRDAAPYTPPNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Species: variola virus
C;Becies: variola wirus
C;Accession: D36858; S46888; S32385; S35987
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G2R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 15-Sep-2003
C;Accession: D72175
                                                                                                                                                                                                                                                                                                     68 CNKTSDTVCADCEASWYTQVMNQFRTCLS---CSSSCTTDQVEIRACTKQQNRVCACEAG
                                                                                                                                                                                                   8 VALVFELQLWATGHTVPAQVVLTPYKÞEPGYECQISQEYYDRKAQMCCAKCPPGQYVKHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:Y16780; NID:95830555; PIDN:CAB54798.1; PID:95830759
A;Experimental source: strain Garcia-1966
                                                              20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: G2R
C,Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 18.6%; Score 170; DB 2; Length 349; Best Local Similarity 29.0%; Pred. No. 8.3e-07; Matches 38; Conservative 21; Mismatches 64; Indels
                                                                  64; Indels
   Score 173; DB 2,
Pred. No. 6e-07;
                                                              21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    109 WHCT----SEACESCVLHRSCSPGFGV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 RYCALKTHSGSCROCMRLSKCGPGFGV 151
18.9%;
28.6%;
                                                                  42; Conservative
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Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-349 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: D72175
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                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g433831
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homold
F;151-188/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Residues: 1474 (LEWA)
A) Residues: 1474 (LEWA)
A) Cross-references: GB: M60469; NID: 9199827; PIDN: AA39752.1; PID: 9199828
A) Cross-references: GB: M60469; NID: 9199827; PIDN: AA39752.1; PID: 9199828
MOI. Cell. Biol. 11, 3020-3026, 1991
A) Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A) Reference number: A40254; MUID: 91246168; PMID: 1645445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis, factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C;Keywords: Cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-3-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 27-Oct-2003
C;Accession: B38634; A40054; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title Clonling and expression of cDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; MUID:91187885; PMID:1849278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;Kissonerghis, M.; Fellowes, R.; Feldaman, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995.
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 PCGESEFLDTWNRETHCHQHKYCDPNLGL-RVQQKG-TSETDTICTCEEGWHCT----SE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                      C; Accession: 148854
R; Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A; Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A; Reference number: 148854; MUID:95178848; PMID:7873884
                                                    C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LPLOCVLWGCLLTAVHPEPPTACREKOYLIN---SQCCSLCQPGQKLVSDCTEFTETECL
                               gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 174.5; DB 2; 29.9%; Pred. No. 4.4e-07; tive 20; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;166-203/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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Reference number: $54816
Accession: $54816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                          A,Molecule_type: mRNA
A;Residues: 1-459 <RES>
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A; Residues: 1-474 <GOO>
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Residues: 1-22 <KIS>
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hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Cot-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin,
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus c
A;Accession: T28623
A;Accession: T28623
A;Accession: T28623
A;Accession: T28623
A;Molecule type: DNA
A;Residues: 1-348 cMAS>
A;Residues: 1-348 cMAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladeeh 1975
C;Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology
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   glycoprotein; homodimer; phosphoprotein; receptor; surface antig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TFTSRNNHLPPACLSCNGRCNSN---QVETRSCNTTHNRICECSPGYYCLLKGSSGCKACV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LOCVLWGCLLTAVHPEPPTACREKOYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVLWGCLLTAVHPEPPTACREKQYLINSQ-CCSLCQPGQKLVSDCTEFTET-ECLPC--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 CVL-GTLVGLSATPAPKSCPERHYWAQGKLCCQMCEPGTFLVXDCDQHRKTAQCDPC1PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 VS-FSPDHHTRPHCESCRHC--NSGLLV-RNCTITANAECACRNGWQCRDKECTEC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ESEFLDTWNRETHCHQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACESC 119
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                               F)1-20/Domain: signal sequence #status predicted <SIG>F;21-260/Product: CD27 antigen #status predicted <MAT>F;21-29/Domain: extracellular #status predicted <MAT>F;21-39/Domain: NGF receptor repeat homology <NG2>F;27-63/Domain: NGF receptor repeat homology <NG2>F;65-105/Domain: NGF receptor repeat homology <NG2>F;65-105/Domain: proline/serine/threonine-rich F;121-188/Region: proline/serine/threonine-rich F;122-211/Domain: intransmembrane #status predicted <TWN>F;212-260/Domain: intranscallular #status predicted <INT>F;95/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Indels
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18.3%; Score 167.5; DB 2
Best Local Similarity 29.8%; Pred. No. 1.3e-06;
Matches 39; Conservative 21; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                             k; Score 167.5; DB 1
k; Pred. No. 1.1e-06;
15; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                     18.3%;
34.5%;
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A,Molecule type: mRNA
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Best Local
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A46517

CD27 antigen precursor - human

N;Alternate names: CD27L receptor; T cell activation antigen CD27

C;Species: Homo septens (man)

C;Species: Homo septens (man)

C;Accession: A46517, A46454

I Immunol. 149, 3937-3943, 1992

A;Title: Genomic organization and chromosomal localization of the human CD27 gene.

A;Reference number: A4617; MUID:93094588; PMID:1334106

A;Reference number: A4617; MUID:93094588; PMID:1334106

A;Reference number: A6517

A;Residues: L266 - LOE2

A;Note: sequence extracted from NCBI backbone (NCBIP:120386)

A;Note: authors propose an alternative repeat pattern

A;Reference number: A46454; J991

A;Title: The T cell activation antigen CD27 is a member of the nerve growth factor/tumor

A;Reference number: A46454; MUID:92013149; PMID:1655907

A;Residues: L586, A', 60-260 < CAM>
A;Resterence number: A46454; MUID:92013149; PMID:1655907

A;Residues: L586, A', 60-260 < CAM>
A;Residues: 
                                                                                                                                                                                                                                                                                                                                                      to overcome the host protective
A;Reference number: $46868
A;Status: S46888
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-349 «KOL»
A;Cross-references: BEBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
B;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host p
A;Reference number: S32385; MUD:93202281; PMID:8384129
A;Residues: 31-168 «SHC»
A;Residues: 31-168 «SHC»
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFLDIWNRETHCHO-HKYCDPNLGLRVQQKGTSET-DIICTCEEGWHCT---SEACESCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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@
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.6%; Score 170; DB 2; Length 349; 29.0%; Pred. No. 8.3e-07;
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A;Introns: 46/1; 90/1; 150/1; 180/1; 220/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 SQTKCGIGYGV 139
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Best Local Similarity
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Search completed: July 21, 2004, 10:07:17 Job time : 17 secs
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                             R)Ochm, A.; Behrmann, II.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich J. Biol. Chem. 267, 10709-10715, 1992
A/Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member A;Reference number: A38142; MUID:92268122; PMID:1375228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: 137383
R;Gascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule A;Reference number: 137383; MUID:95181785; PMID:7533181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: GDB:APT1
A,Cross-references: GDB:132671; OMIM:134637
A,Cross-references: GDB:132671; OMIM:134637
C,Superfamily: 10924.1-10924.1
C,Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology C,Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>F;85-128/Domain: NGF receptor repeat homology <NG4>F;85-128/Domain: transmembrane #status predicted <IMM>
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C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 CCSLCQPGQKLVSDCT-EFTETECLPCGE-SEFLDTWNRETHCHQHKYCDPNLGLRVQQK 94
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C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 07-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
A;Residues: 1-335 <ITO>
A;Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
A;Cross-references: B.H.
Submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.1%; Score 165; DB 2; Length 335, 29.2%; Pred. No. 2e-06; ive 18; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; not compared with conceptual translation A;Nolecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 GTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIAVRPKT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Note: sequence extracted from NCBI backbone (NCBIP:103810)
A,Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                                                                                                  A;Residues: 1-335 <KRA>
A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742
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A;Molecule type: mRNA
A;Residues: 1-314 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-134,'Q',136-335 <OEH>
A;Experimental source: SKW6.4 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 CNRQAQTRLMLSVVPRI 159
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Pest Local Similarity 29.5.
34: Conservative
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                                                                                                                  A;Reference number: S24543
A;Accession: S24543
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                            Molecule type: mRNA
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